



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 22, 2025 – 01:35 AM EDT

PDB ID : 8TO3 / pdb_00008to3
Title : EGFR(T790M/V948R) in complex with LN5461
Authors : Chitnis, S.P.; Pham, C.D.; Heppner, D.E.
Deposited on : 2023-08-02
Resolution : 2.49 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

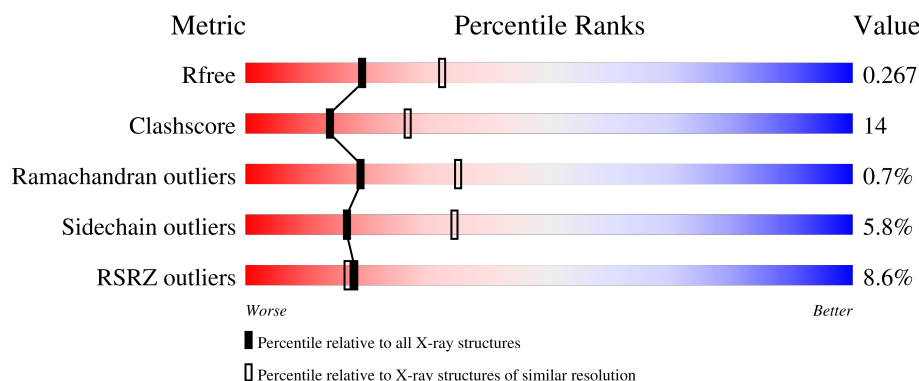
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (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 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	328	
1	B	328	
1	C	328	
1	D	328	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9648 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 Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	293	Total	C	N	O	S	0	0	0
			2355	1514	398	424	19			
1	A	291	Total	C	N	O	S	1	1	0
			2343	1504	402	418	19			
1	B	291	Total	C	N	O	S	4	1	0
			2329	1497	391	422	19			
1	C	295	Total	C	N	O	S	0	1	0
			2372	1524	404	425	19			

There are 8 discrepancies between the modelled and reference sequences:

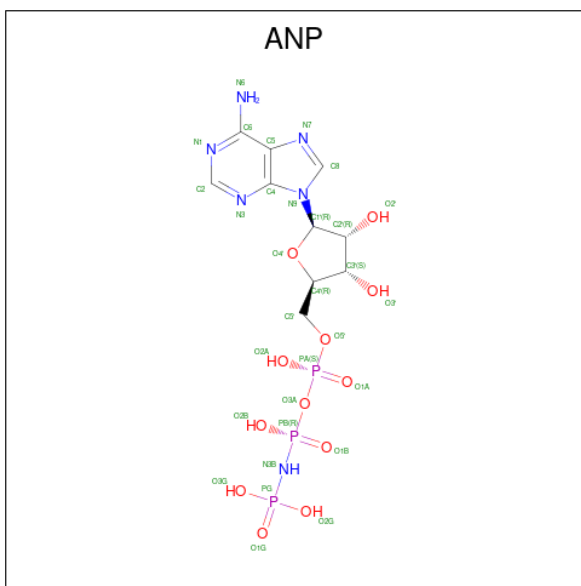
Chain	Residue	Modelled	Actual	Comment	Reference
D	790	MET	THR	engineered mutation	UNP P00533
D	948	ARG	VAL	engineered mutation	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533
C	790	MET	THR	engineered mutation	UNP P00533
C	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		

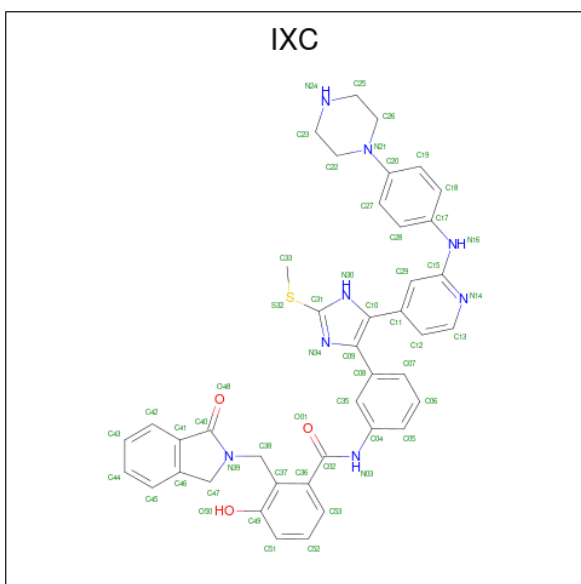
- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID:

ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
3	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
3	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 4 is 3-hydroxy-N-{(3P)-3-[(4P)-2-(methylsulfanyl)-5-{2-[4-(piperazin-1-yl)anilino]pyridin-4-yl}-1H-imidazol-4-yl]phenyl}-2-[(1-oxo-1,3-dihydro-2H-isoindol-2-yl)methyl]benzamide (CCD ID: IXC) (formula: C₄₁H₃₈N₈O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			53	41	8	3	1		

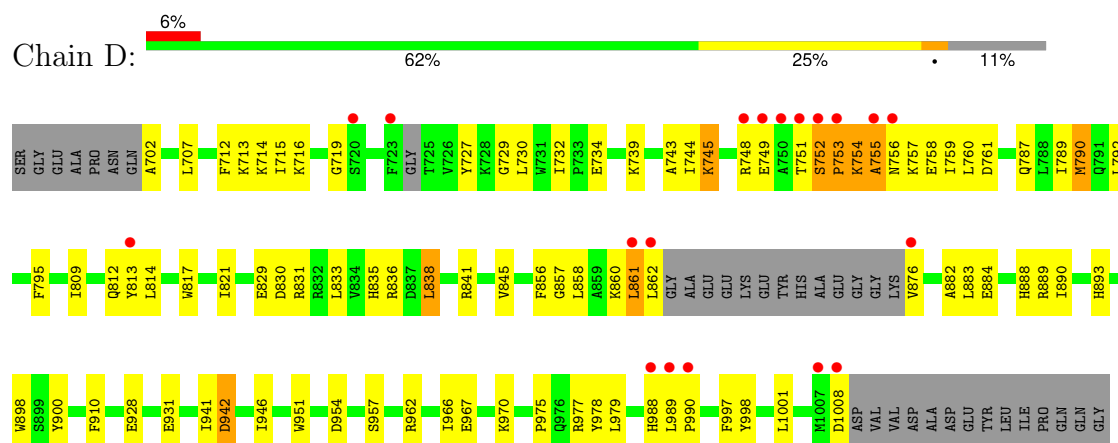
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	32	Total	O	0	0
			32	32		
5	A	17	Total	O	0	0
			17	17		
5	B	27	Total	O	0	0
			27	27		
5	C	24	Total	O	0	0
			24	24		

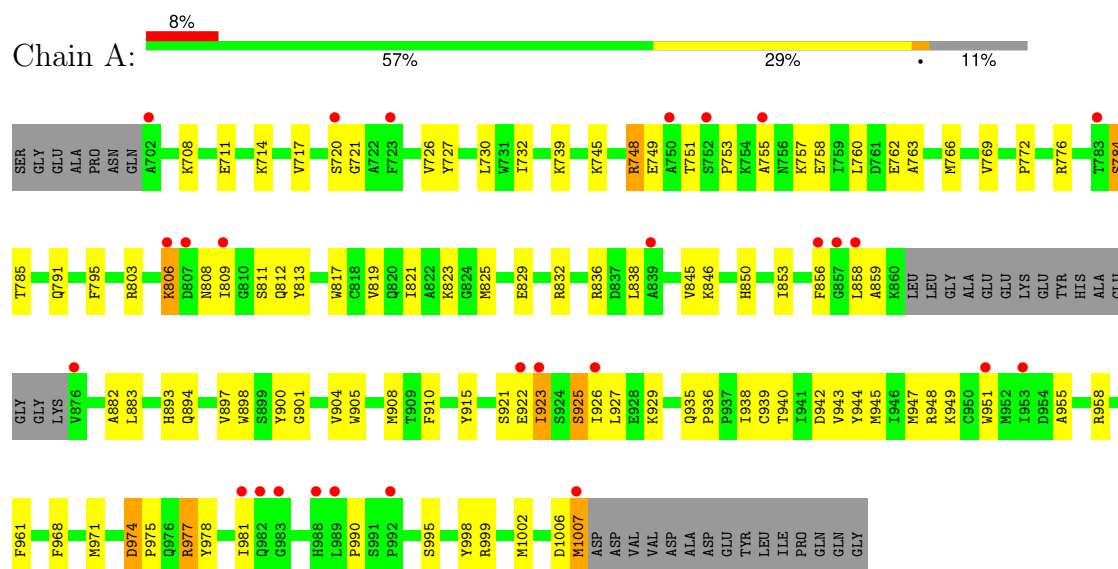
3 Residue-property plots

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: Epidermal growth factor receptor

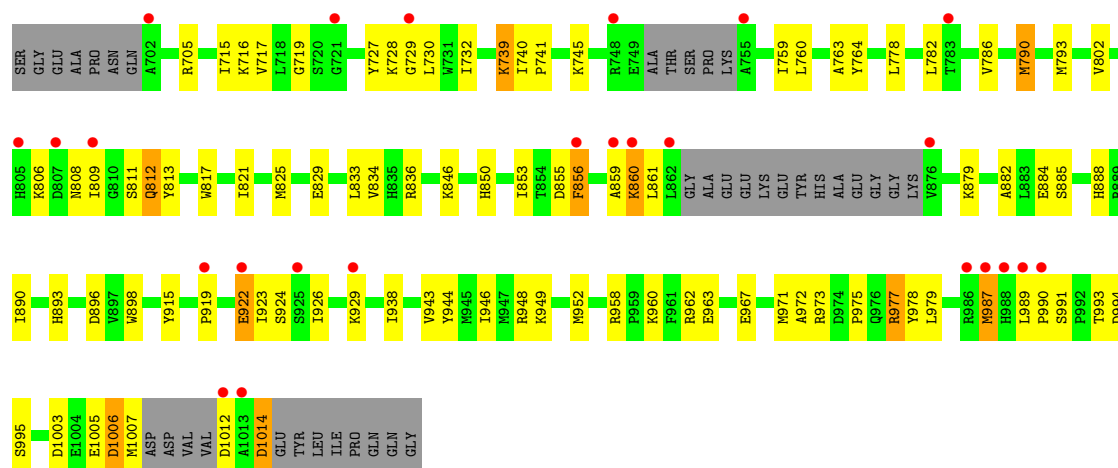


• Molecule 1: Epidermal growth factor receptor

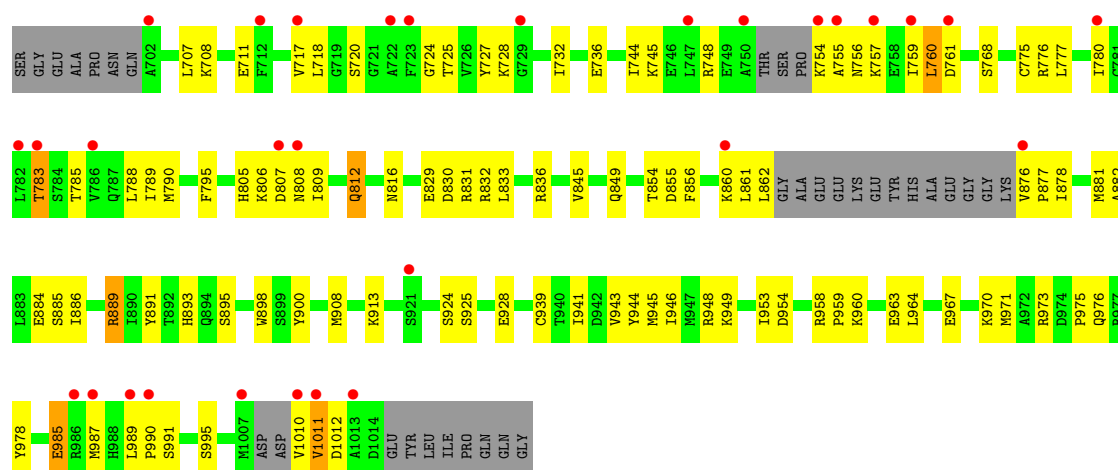


• Molecule 1: Epidermal growth factor receptor





● Molecule 1: Epidermal growth factor receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.00Å 73.37Å 150.59Å 90.00° 99.60° 90.00°	Depositor
Resolution (Å)	56.20 – 2.49 56.20 – 2.49	Depositor EDS
% Data completeness (in resolution range)	98.8 (56.20-2.49) 91.2 (56.20-2.49)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.37 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.229 , 0.269 0.230 , 0.267	Depositor DCC
R_{free} test set	41233 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.521	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9648	wwPDB-VP
Average B, all atoms (Å ²)	49.0	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 23.61 % 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 4.5024e-03. 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: MG, ANP, IXC

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	0/2397	0.70	0/3240
1	B	0.49	0/2381	0.71	0/3218
1	C	0.49	0/2424	0.70	0/3274
1	D	0.51	0/2405	0.70	0/3252
All	All	0.50	0/9607	0.70	0/12984

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	2343	0	2391	81	0
1	B	2329	0	2354	63	0
1	C	2372	0	2417	74	0
1	D	2355	0	2400	61	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	B	31	0	13	2	0
3	C	31	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	31	0	13	3	0
4	A	53	0	0	5	0
5	A	17	0	0	1	0
5	B	27	0	0	3	0
5	C	24	0	0	2	0
5	D	32	0	0	3	0
All	All	9648	0	9601	271	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 14.

All (271) 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:C:946:ILE:HD11	1:C:967:GLU:HG2	1.44	0.98
1:C:759:ILE:HD12	1:C:759:ILE:H	1.38	0.88
1:B:808:ASN:O	1:B:987:MET:SD	2.33	0.87
1:B:730:LEU:HD22	1:B:739:LYS:HB3	1.55	0.86
1:B:1006:ASP:OD1	1:B:1006:ASP:N	2.12	0.83
1:A:812:GLN:HG3	1:A:975:PRO:HG3	1.62	0.81
1:D:861:LEU:HG	1:D:862:LEU:HD22	1.63	0.81
1:A:806:LYS:HE3	1:C:970:LYS:HG3	1.60	0.81
1:D:707:LEU:HD13	1:D:789:ILE:HD13	1.65	0.79
1:C:756:ASN:HA	1:C:759:ILE:HD13	1.62	0.79
1:C:849:GLN:HG2	1:C:990:PRO:HG2	1.65	0.78
1:A:971:MET:HG2	1:A:978:TYR:CD2	2.19	0.77
1:B:879:LYS:HG2	1:B:915:TYR:HD2	1.51	0.74
1:D:889:ARG:HG2	1:D:889:ARG:HH11	1.55	0.72
1:D:941:ILE:HD12	1:D:942:ASP:N	2.05	0.72
1:D:730:LEU:HD22	1:D:739:LYS:HB3	1.71	0.71
1:B:960:LYS:H	1:B:963:GLU:HG3	1.55	0.71
1:A:971:MET:HA	1:A:978:TYR:HE2	1.56	0.70
1:B:943:VAL:HG22	1:B:971:MET:HE1	1.74	0.69
1:A:905:TRP:HD1	1:A:947:MET:HE1	1.57	0.69
1:B:813:TYR:CE2	1:B:990:PRO:HD3	2.28	0.69
1:D:732:ILE:HG13	1:D:739:LYS:HG3	1.74	0.68
1:B:884:GLU:OE2	1:B:958:ARG:NH2	2.26	0.67
1:D:942:ASP:O	1:D:946:ILE:HG13	1.95	0.67
1:D:715:ILE:HG22	1:D:716:LYS:HG2	1.76	0.66
1:A:971:MET:HA	1:A:978:TYR:CE2	2.30	0.66
1:C:759:ILE:HG23	1:C:861:LEU:HD11	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:809:ILE:HB	1:A:910:PHE:HE1	1.61	0.66
1:A:945:MET:O	1:A:949:LYS:HG3	1.95	0.65
1:A:806:LYS:CE	1:C:970:LYS:HG3	2.27	0.65
1:C:718:LEU:HD21	1:C:728:LYS:HB2	1.78	0.65
1:C:727:TYR:HB2	1:C:744:ILE:HG23	1.78	0.65
1:C:908:MET:HG3	1:C:939:CYS:SG	2.36	0.65
1:C:941:ILE:O	1:C:945:MET:HG3	1.97	0.64
1:C:829:GLU:HG3	1:C:893:HIS:CG	2.32	0.64
1:D:829:GLU:HG3	1:D:893:HIS:CG	2.32	0.64
1:A:968:PHE:HA	1:A:971:MET:HB2	1.78	0.64
1:C:884:GLU:OE1	1:C:958:ARG:NH2	2.28	0.64
1:B:829:GLU:HG3	1:B:893:HIS:CG	2.33	0.63
1:D:702:ALA:N	5:D:1201:HOH:O	2.31	0.62
1:D:754:LYS:O	1:D:756:ASN:N	2.33	0.62
1:D:755:ALA:HA	1:D:758:GLU:HG2	1.81	0.62
1:D:739:LYS:NZ	5:D:1202:HOH:O	2.31	0.61
1:A:935:GLN:NE2	1:A:939:CYS:O	2.32	0.61
1:A:898:TRP:HE3	1:A:958:ARG:NH1	1.99	0.60
1:C:707:LEU:HD12	1:C:789:ILE:HD13	1.82	0.60
3:C:1102:ANP:H5'2	3:C:1102:ANP:H8	1.81	0.60
1:A:769:VAL:HG11	1:A:856:PHE:CZ	2.37	0.60
1:B:836:ARG:HH11	1:B:859:ALA:HB1	1.66	0.60
1:B:879:LYS:HG2	1:B:915:TYR:CD2	2.35	0.60
1:C:768:SER:OG	1:C:831:ARG:NH2	2.27	0.59
1:A:748:ARG:HG3	1:A:749:GLU:H	1.68	0.59
1:A:995:SER:O	1:A:999:ARG:HG3	2.03	0.58
1:A:940:THR:HG22	1:A:942:ASP:H	1.69	0.58
1:C:973:ARG:NH2	5:C:1203:HOH:O	2.36	0.58
1:C:924:SER:O	1:C:928:GLU:HG3	2.04	0.58
1:A:922:GLU:O	1:A:926:ILE:HG23	2.02	0.58
1:A:717:VAL:HG21	1:C:830:ASP:HB3	1.86	0.57
1:B:943:VAL:HG22	1:B:971:MET:CE	2.33	0.57
1:A:813:TYR:OH	1:A:990:PRO:HD3	2.05	0.57
1:A:971:MET:HG2	1:A:978:TYR:CE2	2.40	0.57
1:B:745:LYS:NZ	1:B:855:ASP:OD2	2.37	0.57
1:B:926:ILE:HA	1:B:929:LYS:HD3	1.86	0.57
1:D:833:LEU:HB3	1:D:856:PHE:CZ	2.40	0.57
1:C:783:THR:HB	1:C:785:THR:H	1.70	0.56
1:D:830:ASP:HB3	1:B:717:VAL:HG21	1.86	0.56
1:D:883:LEU:HD21	1:D:928:GLU:HG3	1.86	0.56
1:D:941:ILE:HD12	1:D:942:ASP:H	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:MET:HG2	1:A:961:PHE:CZ	2.41	0.56
1:D:888:HIS:HB2	1:D:890:ILE:HG13	1.87	0.56
1:A:730:LEU:HD22	1:A:739:LYS:HB3	1.88	0.55
1:C:943:VAL:HG22	1:C:971:MET:HE1	1.88	0.55
1:D:809:ILE:HB	1:D:910:PHE:HE1	1.72	0.55
1:C:812:GLN:HG2	1:C:975:PRO:HG3	1.87	0.55
1:A:898:TRP:O	1:A:901:GLY:N	2.40	0.55
1:A:915:TYR:CG	1:A:923:ILE:HD11	2.43	0.54
1:B:719:GLY:HA3	3:B:1102:ANP:H4'	1.88	0.54
1:D:841:ARG:HD2	3:D:1102:ANP:HNB1	1.72	0.54
1:A:938:ILE:HD12	1:A:981:ILE:HD11	1.89	0.54
1:C:708:LYS:O	1:C:711:GLU:HG2	2.08	0.54
1:D:831:ARG:O	1:D:833:LEU:HD22	2.08	0.54
1:A:811:SER:OG	1:A:975:PRO:HB2	2.07	0.54
1:A:819:VAL:HG12	1:A:823:LYS:HE2	1.89	0.54
1:D:759:ILE:HD13	1:D:861:LEU:HD13	1.90	0.53
1:B:993:THR:HG23	5:B:1218:HOH:O	2.08	0.53
1:D:795:PHE:HB2	1:D:845:VAL:O	2.09	0.53
1:B:846:LYS:NZ	1:B:1005:GLU:OE2	2.40	0.53
1:C:836:ARG:HG2	1:C:891:TYR:CD1	2.43	0.53
1:C:816:ASN:ND2	1:C:1010:VAL:O	2.42	0.53
1:C:946:ILE:CD1	1:C:967:GLU:HG2	2.29	0.53
1:A:898:TRP:CE3	1:A:951:TRP:HA	2.44	0.53
1:B:971:MET:HE3	1:B:978:TYR:CD2	2.44	0.53
1:B:759:ILE:HD12	1:B:786:VAL:HG21	1.91	0.52
1:D:719:GLY:HA3	3:D:1102:ANP:H4'	1.90	0.52
1:C:990:PRO:O	1:C:991:SER:HB2	2.09	0.52
1:A:748:ARG:HH21	1:C:832:ARG:HD2	1.74	0.52
1:B:778:LEU:HG	1:B:790:MET:HA	1.91	0.52
1:B:885:SER:HB3	1:B:890:ILE:O	2.09	0.52
1:B:850:HIS:ND1	1:B:1003:ASP:OD2	2.43	0.52
1:C:757:LYS:HA	1:C:760:LEU:HB2	1.91	0.52
1:C:944:TYR:CZ	1:C:948:ARG:HD3	2.44	0.52
1:A:821:ILE:HG23	1:A:853:ILE:HD11	1.92	0.52
1:A:974:ASP:O	1:A:977:ARG:HB3	2.09	0.52
1:C:971:MET:HG2	1:C:978:TYR:CG	2.44	0.52
1:B:829:GLU:HG3	1:B:893:HIS:CD2	2.45	0.52
1:D:962:ARG:CZ	1:D:962:ARG:HB3	2.39	0.52
1:A:900:TYR:O	1:A:904:VAL:HG23	2.10	0.52
1:D:889:ARG:HG2	1:D:889:ARG:NH1	2.25	0.51
1:A:858:LEU:HD23	4:A:1101:IXC:C42	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:748:ARG:HG3	1:A:749:GLU:N	2.25	0.51
1:A:905:TRP:CD1	1:A:947:MET:HE1	2.41	0.51
1:B:960:LYS:N	1:B:963:GLU:HG3	2.24	0.51
1:C:744:ILE:HD12	1:C:788:LEU:O	2.11	0.51
1:C:759:ILE:H	1:C:759:ILE:CD1	2.18	0.51
1:D:817:TRP:O	1:D:821:ILE:HG13	2.10	0.51
1:A:943:VAL:HG22	1:A:971:MET:CE	2.41	0.51
1:C:882:ALA:HA	1:C:898:TRP:CD2	2.45	0.51
1:D:841:ARG:HD2	3:D:1102:ANP:N3B	2.26	0.50
1:A:925:SER:O	1:A:929:LYS:HD3	2.11	0.50
1:A:856:PHE:O	4:A:1101:IXC:O50	2.29	0.50
1:A:977:ARG:O	1:A:977:ARG:HG3	2.12	0.50
1:A:955:ALA:HA	1:A:958:ARG:HE	1.77	0.50
1:C:878:ILE:HD12	1:C:886:ILE:HG23	1.93	0.50
1:D:714:LYS:HD3	1:D:727:TYR:CD1	2.47	0.50
1:D:813:TYR:OH	1:D:990:PRO:HD3	2.11	0.50
1:A:748:ARG:NH2	1:C:832:ARG:HD2	2.26	0.50
1:D:753:PRO:HB2	1:C:953:ILE:HG21	1.93	0.49
1:D:946:ILE:CD1	1:D:967:GLU:HG2	2.42	0.49
1:A:998:TYR:HD1	1:A:1002:MET:HE2	1.77	0.49
1:A:751:THR:OG1	1:A:755:ALA:HB3	2.11	0.49
1:B:882:ALA:HA	1:B:898:TRP:CD2	2.47	0.49
1:B:929:LYS:HE2	5:B:1202:HOH:O	2.12	0.49
1:C:760:LEU:HD11	1:C:780:ILE:HG21	1.95	0.49
1:C:885:SER:O	1:C:889:ARG:NH1	2.45	0.49
1:B:812:GLN:OE1	1:B:1012:ASP:HB3	2.13	0.49
1:B:802:VAL:HA	1:B:809:ILE:HD11	1.94	0.49
1:C:754:LYS:CB	1:C:759:ILE:HD11	2.43	0.49
1:B:825:MET:SD	1:B:853:ILE:HD13	2.53	0.49
1:B:919:PRO:HG2	1:B:922[B]:GLU:HB2	1.95	0.49
1:C:854:THR:OG1	1:C:855:ASP:N	2.47	0.48
1:D:946:ILE:HD13	1:D:967:GLU:HG2	1.94	0.48
1:A:836:ARG:HD3	1:A:859:ALA:HB3	1.94	0.48
1:D:714:LYS:HE3	1:D:787:GLN:OE1	2.12	0.48
1:A:766:MET:HE1	4:A:1101:IXC:C47	2.43	0.48
1:A:766:MET:HG2	1:A:856:PHE:CE2	2.48	0.48
1:A:829:GLU:HG3	1:A:893:HIS:CD2	2.48	0.48
1:A:955:ALA:HA	1:A:958:ARG:NE	2.28	0.48
1:C:836:ARG:HG2	1:C:891:TYR:CG	2.48	0.48
1:D:836:ARG:CZ	1:D:860:LYS:HG2	2.43	0.48
1:C:971:MET:HG2	1:C:978:TYR:CD1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:812:GLN:CD	1:B:1012:ASP:HB3	2.34	0.48
1:B:972:ALA:O	1:B:975:PRO:HD3	2.13	0.48
1:A:726:VAL:HG21	4:A:1101:IXC:N34	2.29	0.48
1:C:755:ALA:O	1:C:756:ASN:C	2.53	0.48
1:D:732:ILE:CG1	1:D:739:LYS:HG3	2.44	0.47
1:D:757:LYS:O	1:D:761:ASP:N	2.30	0.47
1:D:790:MET:HE3	5:D:1206:HOH:O	2.13	0.47
1:B:782:LEU:HD22	1:B:786:VAL:HG22	1.95	0.47
1:B:938:ILE:HG12	5:B:1208:HOH:O	2.14	0.47
1:A:791:GLN:OE1	1:A:846:LYS:NZ	2.46	0.47
1:B:922[B]:GLU:O	1:B:926:ILE:HG12	2.13	0.47
1:D:752:SER:C	1:D:754:LYS:H	2.17	0.47
1:B:715:ILE:HG12	1:B:729:GLY:HA2	1.95	0.47
1:D:729:GLY:HA3	1:D:744:ILE:HD12	1.97	0.47
1:A:714:LYS:HD2	1:A:727:TYR:CD1	2.49	0.47
1:B:923:ILE:HD13	1:B:926:ILE:HD11	1.97	0.46
1:A:944:TYR:OH	1:A:948:ARG:NH1	2.42	0.46
1:A:753:PRO:O	1:A:757:LYS:HG3	2.16	0.46
1:C:717:VAL:HG22	1:C:727:TYR:CE2	2.50	0.46
1:B:949:LYS:O	1:B:952:MET:HG3	2.15	0.46
1:D:712:PHE:O	1:D:713:LYS:HD3	2.16	0.46
1:A:829:GLU:HG3	1:A:893:HIS:CG	2.51	0.46
1:B:813:TYR:HE2	1:B:989:LEU:HB2	1.80	0.46
1:C:808:ASN:OD1	1:C:808:ASN:N	2.49	0.46
1:A:908:MET:HG3	1:A:939:CYS:SG	2.56	0.46
1:B:991:SER:HB2	1:B:994:ASP:OD2	2.15	0.46
1:D:989:LEU:HB3	1:D:990:PRO:HD2	1.97	0.46
1:C:861:LEU:HD23	1:C:862:LEU:HG	1.98	0.46
1:B:745:LYS:NZ	3:B:1102:ANP:O1A	2.47	0.46
1:D:752:SER:O	1:D:754:LYS:N	2.50	0.45
1:B:836:ARG:HD2	1:B:860:LYS:HE3	1.98	0.45
1:B:946:ILE:HD11	1:B:967:GLU:HG2	1.98	0.45
1:D:835:HIS:O	1:D:836:ARG:HB2	2.15	0.45
1:A:784:SER:OG	1:A:785:THR:N	2.49	0.45
1:A:883:LEU:HD13	1:A:927:LEU:HB2	1.98	0.45
1:C:833:LEU:HB3	1:C:856:PHE:CZ	2.51	0.45
1:D:809:ILE:HG22	1:D:814:LEU:HG	1.97	0.45
1:A:817:TRP:O	1:A:821:ILE:HG13	2.16	0.45
1:A:803:ARG:NH1	5:A:1202:HOH:O	2.30	0.45
1:B:811:SER:OG	1:B:975:PRO:HB2	2.17	0.45
1:C:724:GLY:HA2	1:C:748:ARG:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:754:LYS:HB2	1:C:759:ILE:HD11	1.99	0.45
1:C:806:LYS:NZ	1:C:807:ASP:OD1	2.45	0.45
1:A:940:THR:HG22	1:A:942:ASP:N	2.31	0.45
1:C:877:PRO:O	1:C:881:MET:HG3	2.15	0.45
1:A:809:ILE:HB	1:A:910:PHE:CE1	2.46	0.45
1:A:948:ARG:HA	1:A:948:ARG:HD2	1.63	0.45
1:A:708:LYS:O	1:A:711:GLU:HG2	2.17	0.45
1:B:944:TYR:CZ	1:B:948:ARG:HD3	2.52	0.45
1:C:985:GLU:H	1:C:985:GLU:HG2	1.53	0.44
1:B:760:LEU:HD13	1:B:764:TYR:HE2	1.82	0.44
1:B:760:LEU:HA	1:B:763:ALA:HB3	1.99	0.44
1:C:732:ILE:HD11	1:C:736:GLU:O	2.17	0.44
1:A:894:GLN:O	1:A:897:VAL:HG12	2.17	0.44
1:A:971:MET:HG2	1:A:978:TYR:HD2	1.79	0.44
1:C:900:TYR:CE1	1:C:964:LEU:HD13	2.53	0.44
1:B:888:HIS:HB2	1:B:890:ILE:HG13	2.00	0.44
1:B:977:ARG:HD2	1:B:978:TYR:CE1	2.53	0.44
1:D:888:HIS:HB2	1:D:890:ILE:CG1	2.46	0.44
1:B:717:VAL:HG22	1:B:727:TYR:CE2	2.53	0.44
1:B:732:ILE:HD11	1:B:739:LYS:HG3	2.00	0.44
1:B:817:TRP:O	1:B:821:ILE:HG13	2.18	0.44
1:D:754:LYS:HE3	1:C:954:ASP:HA	2.00	0.43
1:D:884:GLU:HB2	1:D:890:ILE:HD12	1.99	0.43
1:A:732:ILE:HG12	1:A:739:LYS:NZ	2.33	0.43
1:D:857:GLY:O	1:D:861:LEU:HD23	2.19	0.43
1:A:898:TRP:CE3	1:A:958:ARG:NH1	2.84	0.43
1:D:997:PHE:CZ	1:D:1001:LEU:HD11	2.53	0.43
1:A:745:LYS:HB2	4:A:1101:IXC:C06	2.49	0.43
1:B:833:LEU:HD13	1:B:856:PHE:CE2	2.54	0.43
1:D:812:GLN:HG3	1:D:975:PRO:HG2	2.01	0.43
1:A:819:VAL:CG1	1:A:823:LYS:HE2	2.47	0.43
1:C:795:PHE:HB2	1:C:845:VAL:O	2.19	0.43
1:C:876:VAL:HG12	1:C:881:MET:CE	2.49	0.43
1:A:821:ILE:HA	1:A:853:ILE:HD11	2.00	0.42
1:B:879:LYS:HE2	1:B:915:TYR:HB2	2.01	0.42
1:D:743:ALA:HB2	1:D:792:LEU:HA	2.01	0.42
1:A:772:PRO:O	1:A:850:HIS:NE2	2.52	0.42
1:C:720:SER:HA	1:C:725:THR:HA	2.01	0.42
1:C:776:ARG:HB2	5:C:1207:HOH:O	2.19	0.42
1:C:948:ARG:HD2	1:C:948:ARG:HA	1.86	0.42
1:A:720:SER:HB3	1:A:721:GLY:H	1.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:946:ILE:HD11	1:B:967:GLU:CG	2.50	0.42
1:C:745:LYS:NZ	1:C:855:ASP:OD2	2.52	0.42
1:C:971:MET:CE	1:C:978:TYR:HB3	2.49	0.42
1:D:978:TYR:C	1:D:979:LEU:HD22	2.40	0.42
1:A:758:GLU:H	1:A:758:GLU:HG2	1.53	0.42
1:B:973:ARG:HB3	1:B:1014:ASP:HB3	2.01	0.42
1:C:805:HIS:HB2	1:C:809:ILE:HD11	2.01	0.42
1:D:838:LEU:HD13	1:D:900:TYR:HA	2.01	0.42
1:A:748:ARG:HH21	1:C:832:ARG:CD	2.31	0.42
1:A:795:PHE:HB2	1:A:845:VAL:O	2.19	0.42
1:C:777:LEU:HD11	1:C:788:LEU:HB3	2.01	0.42
1:D:966:ILE:O	1:D:970:LYS:HG3	2.19	0.42
1:B:716:LYS:HE2	1:B:728:LYS:HD3	2.02	0.42
1:B:834:VAL:HG13	1:B:896:ASP:OD2	2.20	0.42
1:D:745:LYS:HD3	1:D:858:LEU:HD21	2.01	0.42
1:C:973:ARG:HA	1:C:1012:ASP:O	2.20	0.42
1:A:772:PRO:HG3	1:A:1007:MET:HA	2.01	0.41
1:A:760:LEU:HA	1:A:763:ALA:HB3	2.02	0.41
1:D:898:TRP:CE3	1:D:951:TRP:HA	2.55	0.41
1:A:751:THR:OG1	1:A:755:ALA:CB	2.68	0.41
1:D:954:ASP:OD2	1:D:957:SER:OG	2.39	0.41
1:D:977:ARG:O	1:D:977:ARG:HG2	2.20	0.41
1:C:775:CYS:SG	1:C:854:THR:HB	2.60	0.41
1:C:949:LYS:HB3	1:C:959:PRO:HD3	2.02	0.41
1:D:882:ALA:HA	1:D:898:TRP:CD2	2.55	0.41
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.56	0.41
1:A:944:TYR:CZ	1:A:948:ARG:HD3	2.55	0.41
1:B:836:ARG:HD3	1:B:859:ALA:HB3	2.02	0.41
1:B:978:TYR:O	1:B:979:LEU:HD23	2.21	0.41
1:C:756:ASN:CA	1:C:759:ILE:HD13	2.43	0.41
1:B:960:LYS:HE3	1:B:960:LYS:HB3	1.71	0.40
1:B:740:ILE:HA	1:B:741:PRO:HD3	1.94	0.40
1:C:759:ILE:HD12	1:C:759:ILE:N	2.19	0.40
1:C:889:ARG:HA	1:C:889:ARG:HD3	1.93	0.40
1:C:895:SER:O	1:C:898:TRP:HB3	2.20	0.40
1:D:831:ARG:HB3	1:D:833:LEU:HD23	2.03	0.40
1:A:936:PRO:O	1:A:939:CYS:HB2	2.21	0.40
1:C:876:VAL:HG12	1:C:881:MET:HE3	2.02	0.40
1:C:960:LYS:HB2	1:C:963:GLU:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	288/328 (88%)	270 (94%)	16 (6%)	2 (1%)	19	35
1	B	284/328 (87%)	263 (93%)	20 (7%)	1 (0%)	30	49
1	C	288/328 (88%)	275 (96%)	12 (4%)	1 (0%)	37	56
1	D	287/328 (88%)	269 (94%)	14 (5%)	4 (1%)	9	17
All	All	1147/1312 (87%)	1077 (94%)	62 (5%)	8 (1%)	19	35

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	755	ALA
1	B	806	LYS
1	C	1011	VAL
1	A	806	LYS
1	D	748	ARG
1	A	784	SER
1	D	754	LYS
1	D	753	PRO

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	258/288 (90%)	245 (95%)	13 (5%)	20	41
1	B	256/288 (89%)	238 (93%)	18 (7%)	12	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	261/288 (91%)	246 (94%)	15 (6%)	17	35
1	D	261/288 (91%)	246 (94%)	15 (6%)	17	35
All	All	1036/1152 (90%)	975 (94%)	61 (6%)	17	33

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	734	GLU
1	D	745	LYS
1	D	749	GLU
1	D	751	THR
1	D	752	SER
1	D	760	LEU
1	D	790	MET
1	D	838	LEU
1	D	861	LEU
1	D	876	VAL
1	D	931	GLU
1	D	942	ASP
1	D	988	HIS
1	D	998	TYR
1	D	1008	ASP
1	A	748	ARG
1	A	762	GLU
1	A	776	ARG
1	A	808	ASN
1	A	832	ARG
1	A	838	LEU
1	A	921	SER
1	A	923	ILE
1	A	925	SER
1	A	974	ASP
1	A	977	ARG
1	A	1006	ASP
1	A	1007	MET
1	B	705	ARG
1	B	739	LYS
1	B	790	MET
1	B	793	MET
1	B	812	GLN
1	B	856	PHE

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Mol	Chain	Res	Type
1	B	860	LYS
1	B	861	LEU
1	B	922[A]	GLU
1	B	922[B]	GLU
1	B	924	SER
1	B	962	ARG
1	B	977	ARG
1	B	987	MET
1	B	995	SER
1	B	1006	ASP
1	B	1007	MET
1	B	1014	ASP
1	C	760	LEU
1	C	761	ASP
1	C	783	THR
1	C	790	MET
1	C	812	GLN
1	C	860	LYS
1	C	889	ARG
1	C	913	LYS
1	C	925	SER
1	C	976	GLN
1	C	985	GLU
1	C	987	MET
1	C	989	LEU
1	C	995	SER
1	C	1011	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ANP	D	1102	2	29,33,33	1.13	4 (13%)	31,52,52	1.28	4 (12%)
3	ANP	C	1102	2	29,33,33	1.13	4 (13%)	31,52,52	1.18	3 (9%)
3	ANP	B	1102	2	29,33,33	1.20	4 (13%)	31,52,52	1.32	4 (12%)
4	IXC	A	1101	-	58,60,60	3.02	19 (32%)	72,85,85	2.04	14 (19%)

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
3	ANP	D	1102	2	-	3/14/38/38	0/3/3/3
3	ANP	C	1102	2	-	5/14/38/38	0/3/3/3
3	ANP	B	1102	2	-	6/14/38/38	0/3/3/3
4	IXC	A	1101	-	-	8/28/50/50	0/8/8/8

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1101	IXC	C08-C09	11.77	1.62	1.49
4	A	1101	IXC	C11-C10	10.45	1.60	1.49
4	A	1101	IXC	C31-S32	8.94	1.83	1.75
4	A	1101	IXC	C40-N39	5.31	1.43	1.36
4	A	1101	IXC	C15-N16	4.35	1.46	1.38
4	A	1101	IXC	C41-C40	4.25	1.55	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1102	ANP	PA-O3A	3.80	1.63	1.59
4	A	1101	IXC	C02-N03	3.59	1.46	1.35
4	A	1101	IXC	C20-N21	3.53	1.48	1.38
3	C	1102	ANP	PG-O1G	3.10	1.50	1.46
3	D	1102	ANP	PG-O1G	3.04	1.50	1.46
4	A	1101	IXC	C47-C46	3.04	1.54	1.50
4	A	1101	IXC	C38-C37	2.97	1.56	1.51
4	A	1101	IXC	C17-N16	2.90	1.47	1.40
4	A	1101	IXC	C04-N03	2.70	1.47	1.41
3	C	1102	ANP	PG-N3B	2.66	1.70	1.63
4	A	1101	IXC	C22-N21	2.45	1.50	1.46
4	A	1101	IXC	C19-C18	2.39	1.42	1.38
4	A	1101	IXC	C26-N21	2.39	1.50	1.46
3	C	1102	ANP	PB-N3B	2.31	1.69	1.63
3	B	1102	ANP	PG-N3B	2.31	1.69	1.63
3	B	1102	ANP	PG-O1G	2.25	1.49	1.46
4	A	1101	IXC	C53-C36	-2.25	1.36	1.39
3	B	1102	ANP	PB-N3B	2.22	1.69	1.63
3	D	1102	ANP	PG-N3B	2.18	1.69	1.63
3	D	1102	ANP	PB-O1B	2.16	1.49	1.46
3	D	1102	ANP	PA-O3A	2.16	1.61	1.59
4	A	1101	IXC	C09-N34	-2.14	1.32	1.37
4	A	1101	IXC	C51-C49	-2.11	1.35	1.39
4	A	1101	IXC	C35-C04	-2.05	1.36	1.39
3	C	1102	ANP	PB-O1B	2.01	1.49	1.46

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1101	IXC	C46-C47-N39	12.09	108.11	102.42
3	B	1102	ANP	O1G-PG-N3B	-3.83	106.14	111.77
4	A	1101	IXC	C13-N14-C15	3.60	122.36	117.21
3	C	1102	ANP	O2B-PB-O1B	-3.45	102.47	109.87
3	D	1102	ANP	O1B-PB-N3B	-3.44	106.70	111.77
4	A	1101	IXC	C47-C46-C41	-3.39	107.60	109.73
4	A	1101	IXC	C12-C13-N14	-3.24	120.00	123.97
4	A	1101	IXC	C53-C36-C37	3.15	123.79	119.78
3	C	1102	ANP	O1B-PB-N3B	-2.99	107.36	111.77
3	B	1102	ANP	O2B-PB-O1B	-2.93	103.58	109.87
3	D	1102	ANP	O2B-PB-O1B	-2.85	103.76	109.87
4	A	1101	IXC	C23-C22-N21	2.67	116.19	110.38
4	A	1101	IXC	C47-N39-C40	-2.58	108.42	113.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1101	IXC	C07-C08-C09	2.53	124.72	120.62
3	B	1102	ANP	O3A-PB-N3B	2.52	113.59	106.59
4	A	1101	IXC	C10-C09-N34	-2.42	107.22	113.76
3	B	1102	ANP	O3G-PG-O1G	-2.37	107.51	113.45
4	A	1101	IXC	C29-C15-N14	-2.32	119.88	122.92
3	D	1102	ANP	C4-C5-N7	2.29	111.76	109.34
4	A	1101	IXC	C09-C10-N30	-2.27	107.64	113.76
4	A	1101	IXC	C33-S32-C31	-2.26	100.56	102.25
3	D	1102	ANP	O3G-PG-O1G	-2.13	108.10	113.45
4	A	1101	IXC	C25-N24-C23	2.11	116.37	110.40
3	C	1102	ANP	C5-C6-N6	2.04	123.42	120.31
4	A	1101	IXC	C52-C51-C49	2.01	122.53	120.05

There are no chirality outliers.

All (22) torsion outliers are listed below:

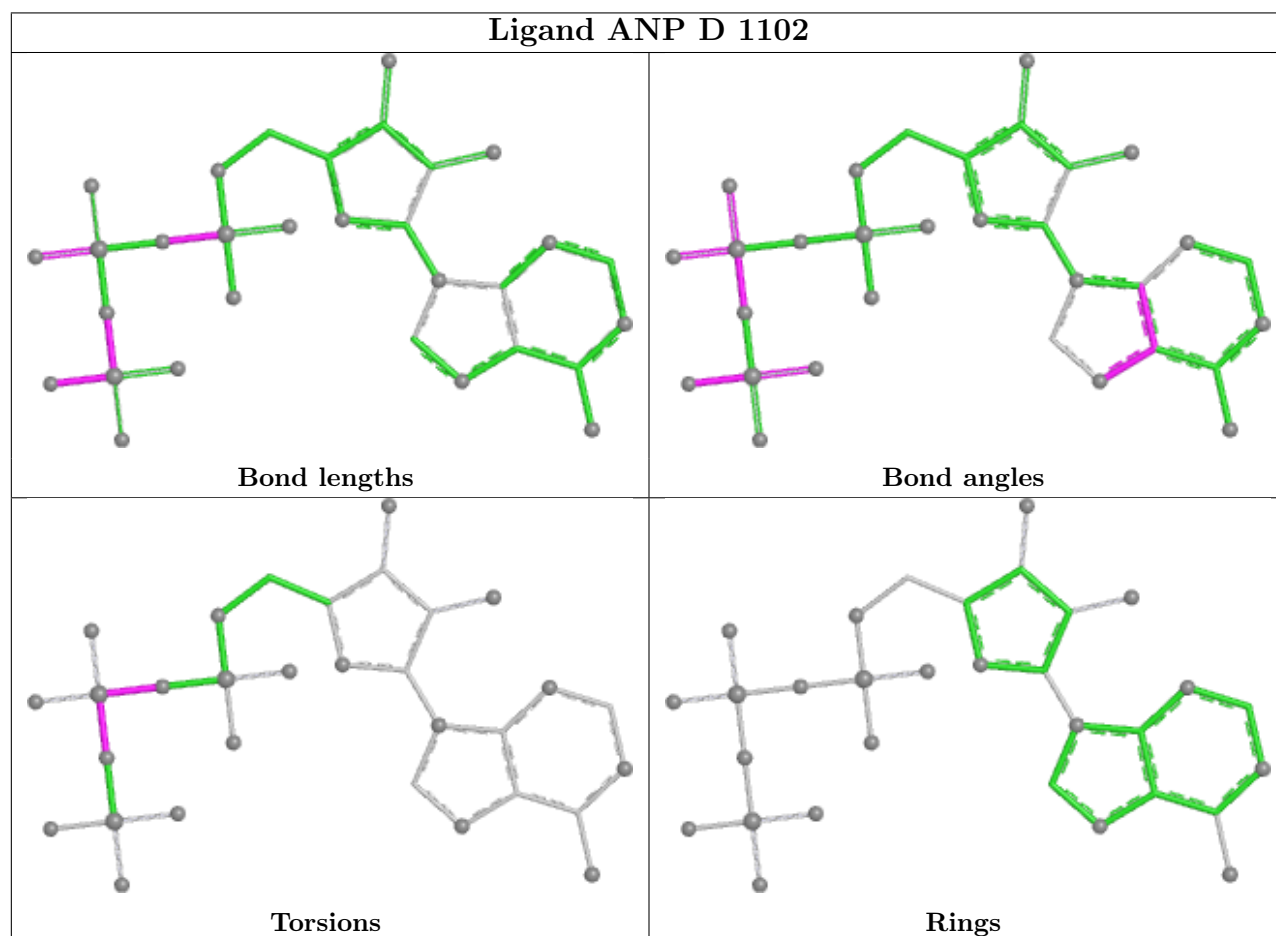
Mol	Chain	Res	Type	Atoms
3	D	1102	ANP	PG-N3B-PB-O1B
3	B	1102	ANP	PB-N3B-PG-O1G
3	B	1102	ANP	PG-N3B-PB-O1B
3	B	1102	ANP	PA-O3A-PB-O2B
3	C	1102	ANP	PG-N3B-PB-O1B
3	C	1102	ANP	PA-O3A-PB-O2B
4	A	1101	IXC	C07-C08-C09-N34
4	A	1101	IXC	C35-C08-C09-N34
4	A	1101	IXC	C27-C20-N21-C22
3	C	1102	ANP	C3'-C4'-C5'-O5'
4	A	1101	IXC	C19-C20-N21-C22
3	C	1102	ANP	O4'-C4'-C5'-O5'
4	A	1101	IXC	C37-C38-N39-C47
3	B	1102	ANP	O4'-C4'-C5'-O5'
3	B	1102	ANP	C3'-C4'-C5'-O5'
3	D	1102	ANP	PA-O3A-PB-O2B
4	A	1101	IXC	O01-C02-C36-C53
4	A	1101	IXC	N03-C02-C36-C53
3	D	1102	ANP	PA-O3A-PB-O1B
3	B	1102	ANP	PA-O3A-PB-O1B
3	C	1102	ANP	PA-O3A-PB-O1B
4	A	1101	IXC	C37-C38-N39-C40

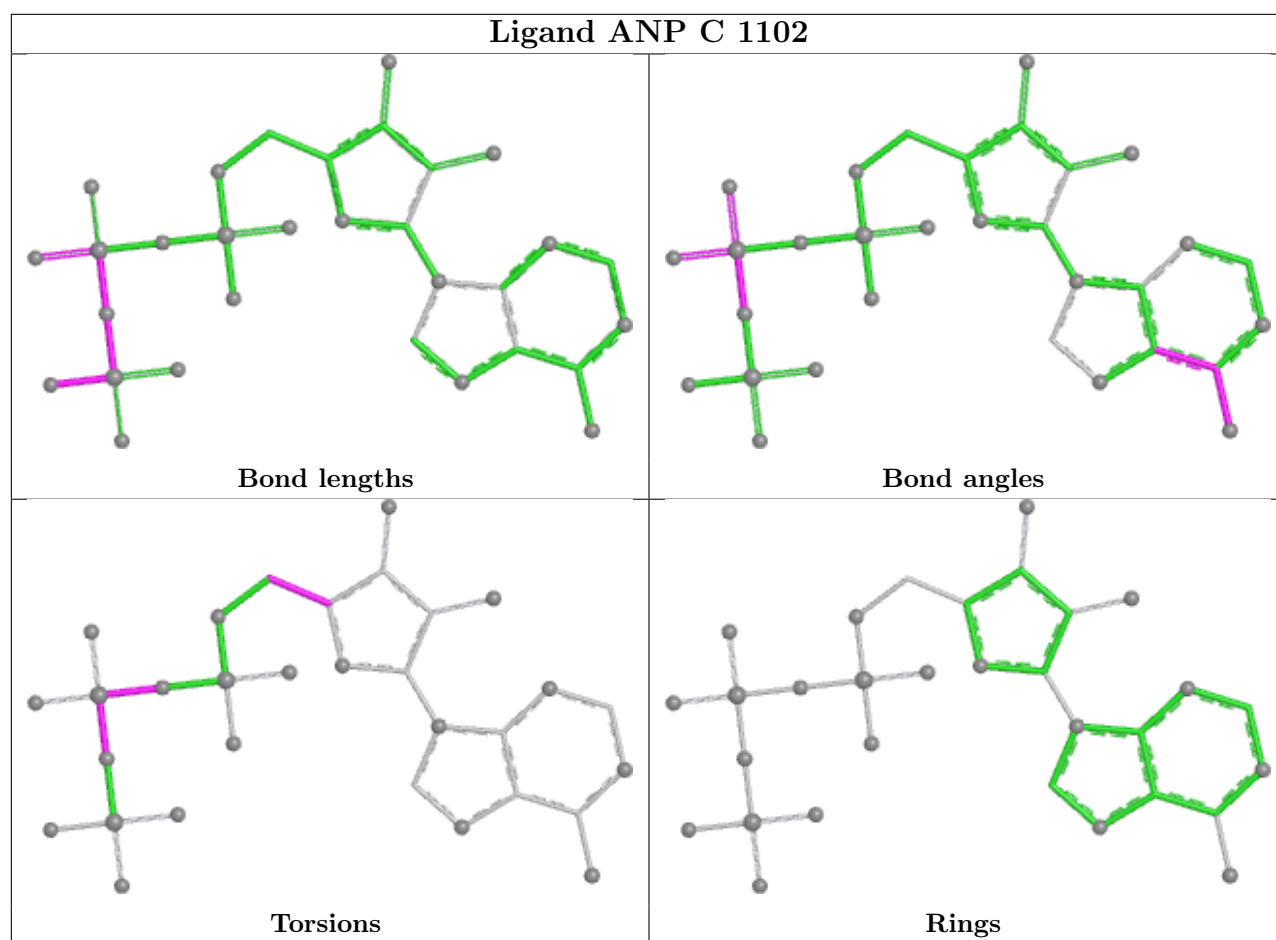
There are no ring outliers.

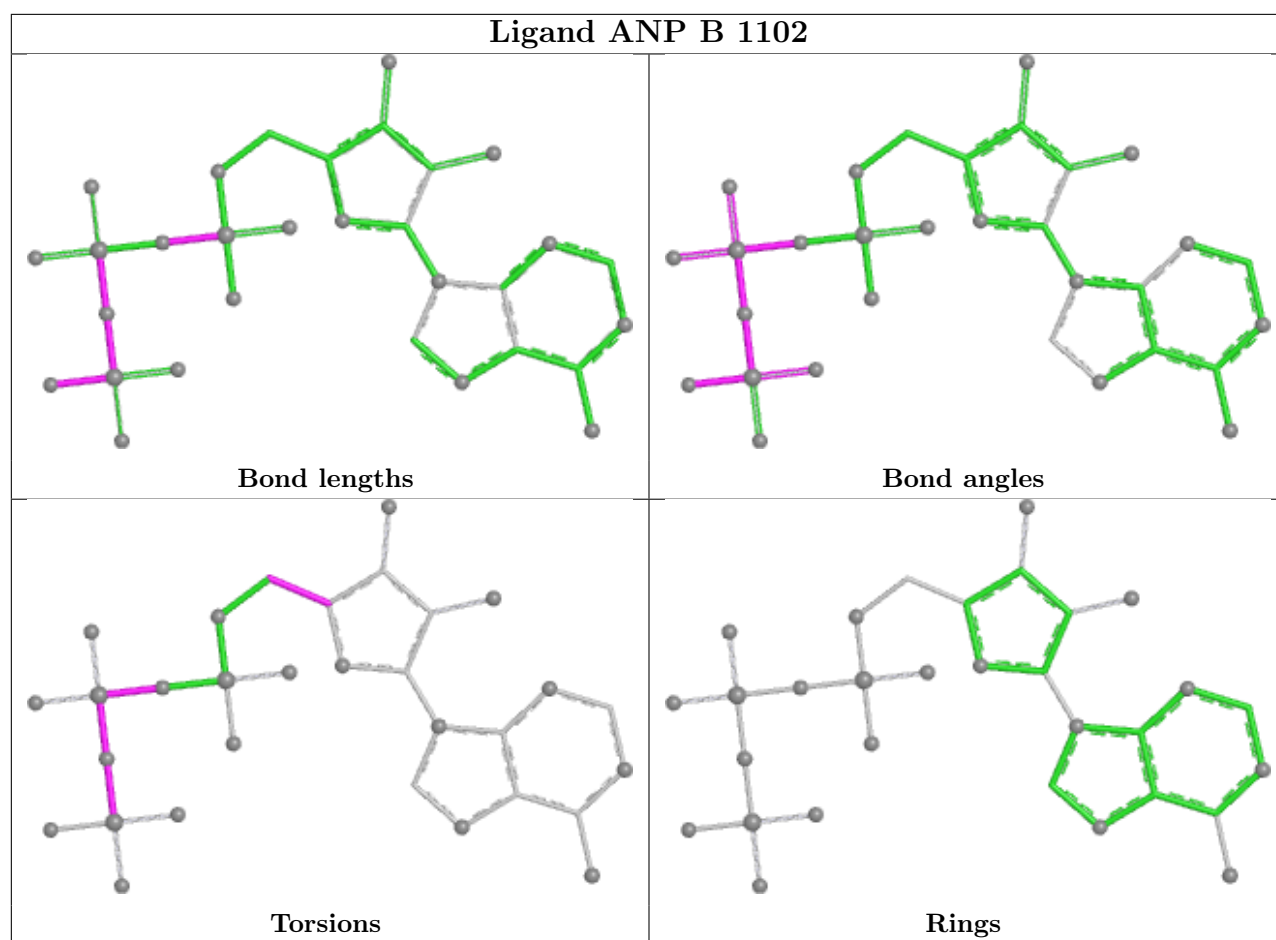
4 monomers are involved in 11 short contacts:

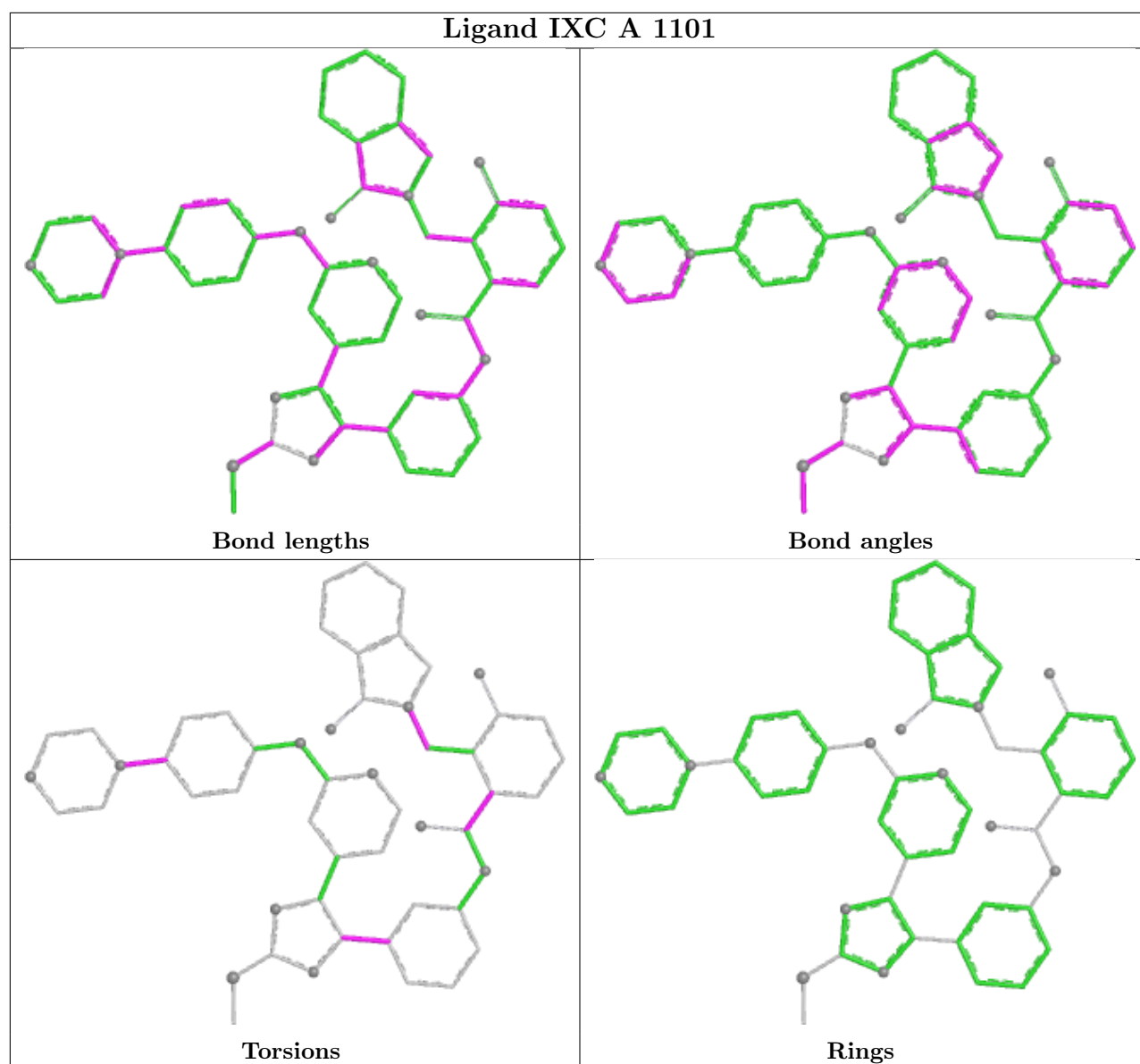
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1102	ANP	3	0
3	C	1102	ANP	1	0
3	B	1102	ANP	2	0
4	A	1101	IXC	5	0

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 [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	291/328 (88%)	0.95	27 (9%)	16 15	28, 53, 78, 97	2 (0%)
1	B	291/328 (88%)	0.76	25 (8%)	18 17	29, 46, 73, 90	1 (0%)
1	C	295/328 (89%)	0.89	30 (10%)	13 13	30, 46, 78, 89	1 (0%)
1	D	293/328 (89%)	0.66	19 (6%)	26 24	30, 43, 71, 84	0
All	All	1170/1312 (89%)	0.81	101 (8%)	18 17	28, 47, 76, 97	4 (0%)

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	990	PRO	4.7
1	B	989	LEU	4.7
1	D	748	ARG	4.7
1	A	982	GLN	4.7
1	B	1013	ALA	4.4
1	B	862	LEU	4.3
1	B	859	ALA	4.3
1	C	755	ALA	4.0
1	C	750	ALA	4.0
1	D	750	ALA	3.9
1	C	757	LYS	3.9
1	C	1010	VAL	3.7
1	C	754	LYS	3.6
1	B	856	PHE	3.6
1	B	807	ASP	3.4
1	B	988	HIS	3.4
1	C	990	PRO	3.3
1	B	721	GLY	3.3
1	B	755	ALA	3.2
1	A	1007	MET	3.2
1	C	702	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	858	LEU	3.2
1	A	857	GLY	3.2
1	B	922[A]	GLU	3.2
1	D	1008	ASP	3.1
1	C	782	LEU	3.1
1	D	990	PRO	3.1
1	C	989	LEU	3.0
1	C	807	ASP	3.0
1	C	1011	VAL	3.0
1	D	862	LEU	3.0
1	A	989	LEU	3.0
1	D	989	LEU	2.9
1	A	923	ILE	2.8
1	C	1007	MET	2.8
1	B	876	VAL	2.8
1	C	783	THR	2.7
1	B	702	ALA	2.7
1	D	755	ALA	2.7
1	A	750	ALA	2.7
1	A	807	ASP	2.7
1	B	987	MET	2.7
1	D	752	SER	2.7
1	C	747	LEU	2.7
1	B	1012	ASP	2.7
1	D	751	THR	2.6
1	B	729	GLY	2.6
1	C	860	LYS	2.6
1	A	953	ILE	2.6
1	A	981	ILE	2.6
1	C	921	SER	2.6
1	C	729	GLY	2.5
1	C	717	VAL	2.5
1	C	786	VAL	2.5
1	C	876	VAL	2.5
1	C	808	ASN	2.5
1	A	988	HIS	2.5
1	A	702	ALA	2.5
1	A	752	SER	2.5
1	D	753	PRO	2.4
1	A	755	ALA	2.4
1	C	987	MET	2.4
1	B	925	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	723	PHE	2.4
1	C	723	PHE	2.4
1	A	992	PRO	2.4
1	B	809	ILE	2.4
1	D	988	HIS	2.3
1	B	929	LYS	2.3
1	B	748	ARG	2.3
1	B	783	THR	2.3
1	C	759	ILE	2.3
1	A	876	VAL	2.3
1	A	723	PHE	2.2
1	C	712	PHE	2.2
1	A	951	TRP	2.2
1	C	722	ALA	2.2
1	D	861	LEU	2.2
1	D	1007	MET	2.2
1	D	720	SER	2.2
1	B	919	PRO	2.2
1	A	922	GLU	2.1
1	C	761	ASP	2.1
1	B	860	LYS	2.1
1	D	876	VAL	2.1
1	A	809	ILE	2.1
1	C	1013	ALA	2.1
1	A	806	LYS	2.1
1	B	805	HIS	2.1
1	C	986	ARG	2.0
1	D	813	TYR	2.0
1	A	926	ILE	2.0
1	C	780	ILE	2.0
1	D	756	ASN	2.0
1	B	986	ARG	2.0
1	A	839	ALA	2.0
1	A	983	GLY	2.0
1	D	749	GLU	2.0
1	A	783	THR	2.0
1	A	856	PHE	2.0
1	A	720	SER	2.0

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

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](#)

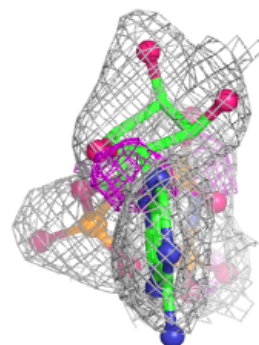
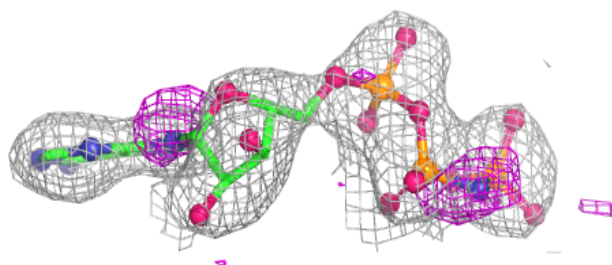
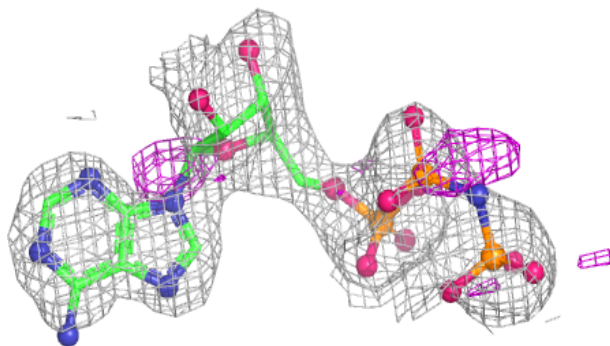
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ANP	C	1102	31/31	0.81	0.12	46,56,66,70	0
4	IXC	A	1101	53/53	0.82	0.18	43,50,65,68	53
3	ANP	D	1102	31/31	0.83	0.12	37,46,51,55	0
3	ANP	B	1102	31/31	0.84	0.10	43,55,63,64	0
2	MG	B	1101	1/1	0.86	0.09	55,55,55,55	0
2	MG	D	1101	1/1	0.92	0.11	45,45,45,45	0
2	MG	C	1101	1/1	0.92	0.07	53,53,53,53	0

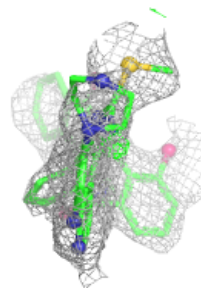
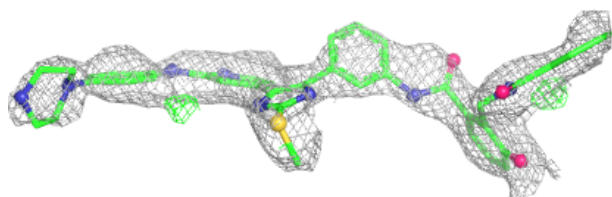
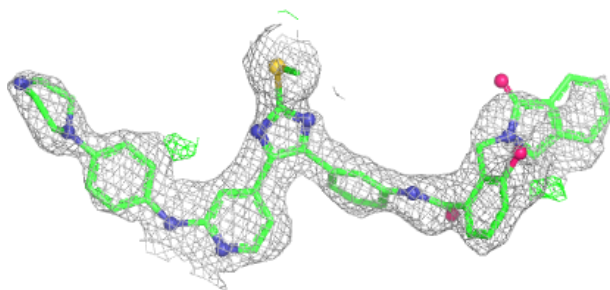
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP C 1102:

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

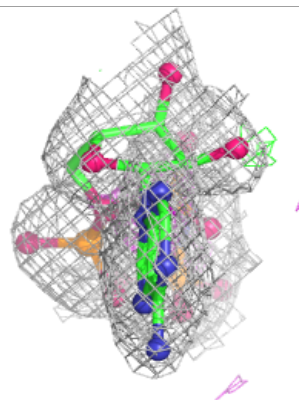
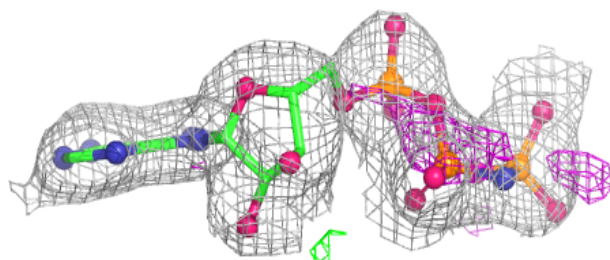
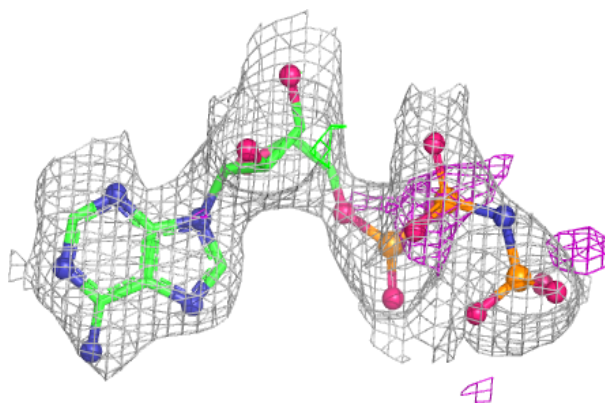
**Electron density around IXC A 1101:**

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

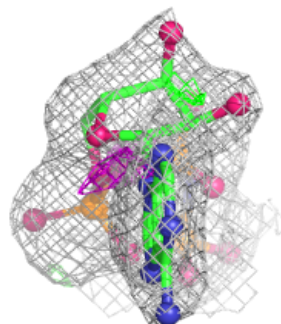
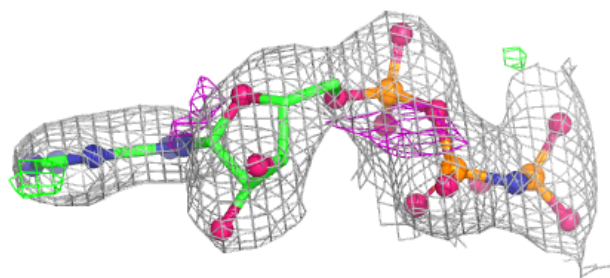
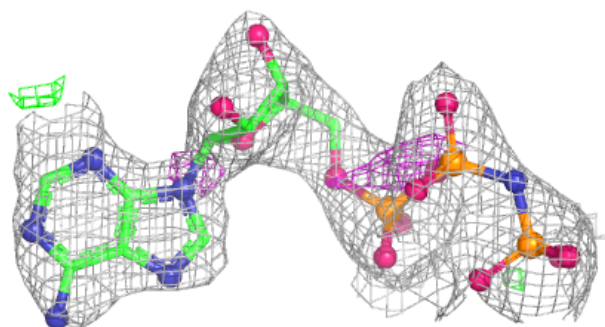


Electron density around ANP D 1102:

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

**Electron density around ANP B 1102:**

$2mF_o-DF_c$ (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.