



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:19 AM UTC

PDB ID : 6WAK / pdb_00006wak
Title : A crystal structure of EGFR(T790M/V948R) in complex with LN3754
Authors : Heppner, D.E.; Eck, M.J.
Deposited on : 2020-03-25
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

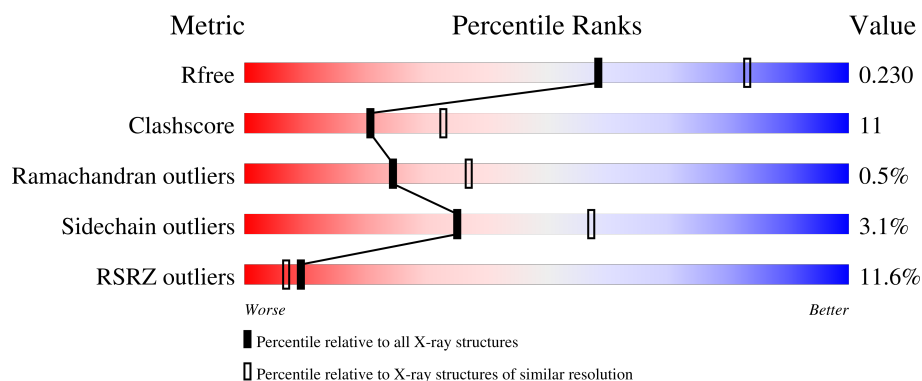
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 $\leq 5\%$. 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	11% 69% 20% 9%
1	B	328	13% 74% 18% • • •
1	C	328	10% 67% 21% • 9%
1	D	328	8% 73% 16% • 9%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10117 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.

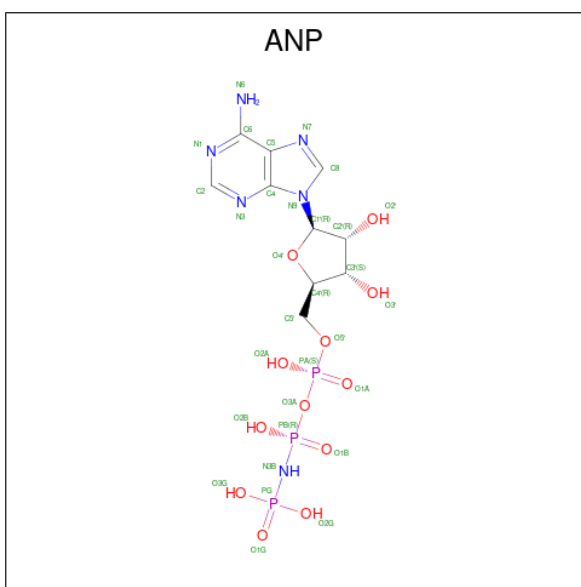
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	297	Total	C	N	O	S	0	1	0
			2404	1542	407	436	19			
1	A	297	Total	C	N	O	S	0	1	0
			2393	1539	407	429	18			
1	B	316	Total	C	N	O	S	0	1	0
			2561	1643	431	468	19			
1	C	299	Total	C	N	O	S	0	1	0
			2410	1542	409	440	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 PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).

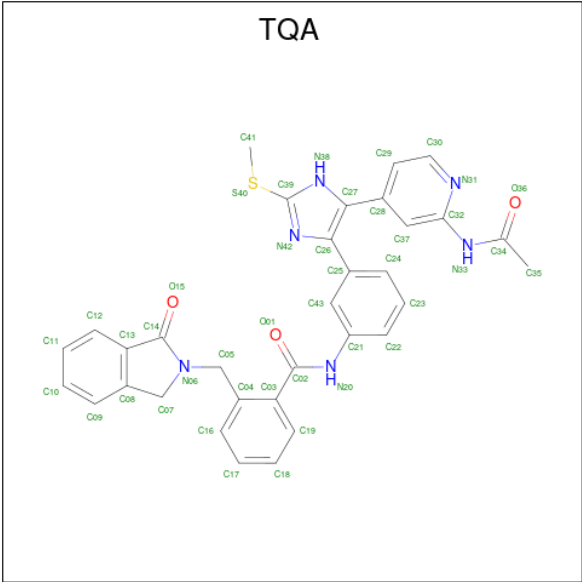


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is N-(3-{5-[2-(acetylamino)pyridin-4-yl]-2-(methylsulfanyl)-1H-imidazol-4-yl}phenyl)-2-[(1-oxo-1,3-dihydro-2H-isoindol-2-yl)methyl]benzamide (CCD ID: TQA) (formula: C₃₃H₂₈N₆O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	S	0	0
			43	33	6	3	1		

- Molecule 5 is water.

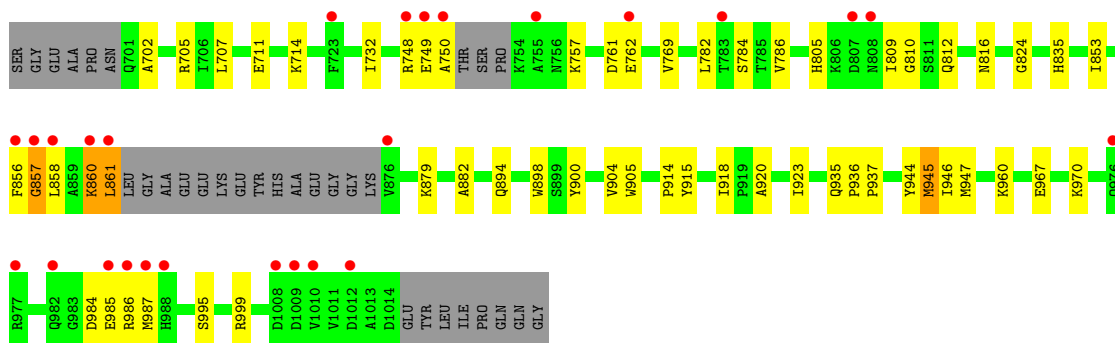
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	51	Total	O	0	0
			51	51		
5	A	48	Total	O	0	0
			48	48		
5	B	71	Total	O	0	0
			71	71		
5	C	40	Total	O	0	0
			40	40		

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.

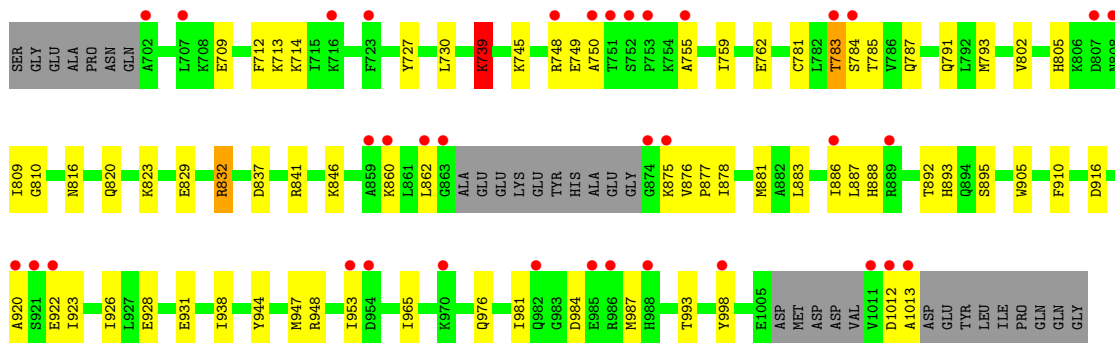
- Molecule 1: Epidermal growth factor receptor

Chain D: 



- Molecule 1: Epidermal growth factor receptor

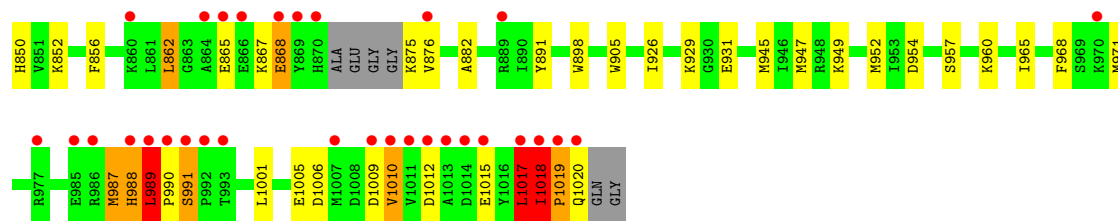
Chain A: 



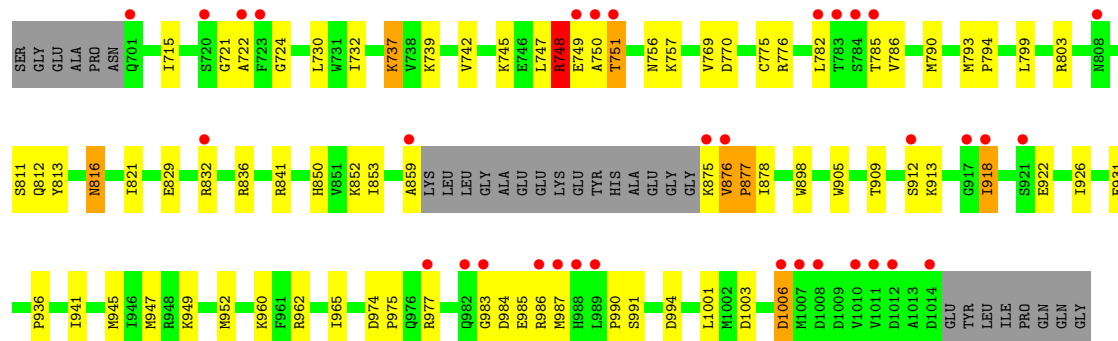
- Molecule 1: Epidermal growth factor receptor

Chain B: 





• 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	72.47Å 103.37Å 87.25Å 90.00° 101.24° 90.00°	Depositor
Resolution (Å)	85.58 – 2.40 85.58 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.5 (85.58-2.40) 92.0 (85.58-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.40Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.218 , 0.230 0.219 , 0.230	Depositor DCC
R_{free} test set	2357 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	10117	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ANP, MG, TQA

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	0.44	1/2444 (0.0%)	0.62	1/3302 (0.0%)
1	B	0.71	8/2617 (0.3%)	0.90	8/3539 (0.2%)
1	C	0.58	5/2461 (0.2%)	0.74	4/3329 (0.1%)
1	D	0.49	2/2454 (0.1%)	0.68	2/3316 (0.1%)
All	All	0.57	16/9976 (0.2%)	0.74	15/13486 (0.1%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1019	PRO	C-O	-8.67	1.12	1.24
1	A	739	LYS	C-O	-7.27	1.15	1.24
1	C	936	PRO	CA-C	7.05	1.55	1.51
1	D	936	PRO	CA-C	7.00	1.55	1.51
1	C	770	ASP	C-O	-6.87	1.16	1.24
1	B	991	SER	C-N	6.57	1.49	1.33
1	C	816	ASN	C-O	-6.38	1.16	1.24
1	B	805	HIS	C-O	-6.07	1.15	1.23
1	D	714	LYS	C-O	-5.70	1.17	1.24
1	C	737	LYS	C-O	-5.70	1.16	1.24
1	B	807	ASP	C-O	-5.65	1.16	1.24
1	B	805	HIS	CE1-NE2	-5.61	1.26	1.32
1	B	756	ASN	C-O	-5.59	1.17	1.24
1	C	877	PRO	C-O	-5.54	1.16	1.24
1	B	988	HIS	CG-ND1	-5.42	1.32	1.38
1	B	806	LYS	C-O	-5.05	1.17	1.24

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	991	SER	CA-C-N	11.04	133.64	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	991	SER	C-N-CA	11.04	133.64	119.84
1	B	991	SER	O-C-N	-7.17	113.08	121.32
1	B	748	ARG	CB-CA-C	-6.97	98.58	110.22
1	B	990	PRO	N-CA-C	-6.10	105.42	113.65
1	B	1018	ILE	N-CA-CB	5.69	119.18	111.21
1	D	857	GLY	N-CA-C	-5.65	108.36	115.08
1	C	748	ARG	N-CA-CB	5.63	118.17	110.01
1	C	936	PRO	O-C-N	5.44	123.81	121.31
1	C	748	ARG	CA-C-N	-5.34	113.70	121.76
1	C	748	ARG	C-N-CA	-5.34	113.70	121.76
1	B	801	TYR	CA-C-O	-5.18	115.38	120.82
1	A	916	ASP	CA-CB-CG	5.17	117.77	112.60
1	D	936	PRO	O-C-N	5.17	123.69	121.31
1	B	1017	LEU	N-CA-C	-5.01	101.00	108.96

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	2393	0	2446	53	0
1	B	2561	0	2590	66	0
1	C	2410	0	2441	64	0
1	D	2404	0	2439	38	0
2	A	31	0	13	1	0
2	B	31	0	13	0	0
2	D	31	0	13	5	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	C	43	0	0	0	0
5	A	48	0	0	4	0
5	B	71	0	0	8	0
5	C	40	0	0	5	0
5	D	51	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10117	0	9955	221	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 11.

All (221) 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:750:ALA:O	1:C:751:THR:HG23	1.34	1.23
1:B:810:GLY:H	1:B:988:HIS:CE1	1.68	1.12
1:C:750:ALA:O	1:C:751:THR:CG2	1.98	1.11
1:B:809:ILE:HA	1:B:988:HIS:HE1	1.25	0.98
1:B:809:ILE:HA	1:B:988:HIS:CE1	1.99	0.98
1:B:810:GLY:N	1:B:988:HIS:CE1	2.32	0.97
1:A:739:LYS:HB3	1:A:739:LYS:NZ	1.80	0.97
1:C:750:ALA:C	1:C:751:THR:HG23	1.93	0.92
1:B:809:ILE:CA	1:B:988:HIS:HE1	1.82	0.92
1:A:781:CYS:SG	1:A:783:THR:HG22	2.15	0.87
1:B:1010:VAL:HG11	1:C:1006:ASP:OD2	1.72	0.87
2:D:1101:ANP:H3'	5:D:1209:HOH:O	1.75	0.86
1:A:739:LYS:HB3	1:A:739:LYS:HZ2	1.36	0.86
1:B:945:MET:HG3	5:B:1267:HOH:O	1.76	0.86
1:B:810:GLY:N	1:B:988:HIS:HE1	1.76	0.81
1:D:702:ALA:HA	1:A:993:THR:HG22	1.62	0.81
1:D:861:LEU:HD13	1:D:861:LEU:N	1.99	0.77
1:C:990:PRO:HB2	1:C:994:ASP:HB2	1.65	0.77
1:D:810:GLY:HA2	1:D:987:MET:HE3	1.66	0.76
1:A:783:THR:OG1	1:A:784:SER:N	2.16	0.75
1:C:785:THR:HA	5:C:1404:HOH:O	1.89	0.72
1:C:782:LEU:HD23	1:C:782:LEU:H	1.54	0.72
1:A:905:TRP:HD1	1:A:947:MET:HE1	1.57	0.69
1:B:749:GLU:HA	5:B:1207:HOH:O	1.92	0.69
1:A:783:THR:OG1	1:A:785:THR:N	2.23	0.69
1:C:909:THR:OG1	1:C:912:SER:HB2	1.92	0.68
1:A:783:THR:HG21	1:A:787:GLN:HE21	1.58	0.68
1:B:809:ILE:C	1:B:988:HIS:HE1	2.01	0.68
1:C:721:GLY:O	1:C:748:ARG:NH1	2.27	0.68
1:A:920:ALA:HA	1:A:923:ILE:HG12	1.74	0.68
1:B:867:LYS:CD	1:B:867:LYS:H	2.06	0.68
1:C:841:ARG:HH12	1:C:877:PRO:HB3	1.59	0.68
1:C:750:ALA:HB1	5:C:1402:HOH:O	1.92	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:829:GLU:O	1:C:832:ARG:HD2	1.94	0.67
2:D:1101:ANP:C3'	5:D:1209:HOH:O	2.38	0.67
1:B:790:MET:SD	5:B:1254:HOH:O	2.52	0.66
1:D:860:LYS:HB2	1:D:861:LEU:HD13	1.78	0.66
1:C:905:TRP:HZ3	1:C:912:SER:O	1.79	0.65
1:A:832:ARG:HG3	1:B:750:ALA:HB3	1.77	0.65
1:B:968:PHE:HA	1:B:971:MET:HE3	1.78	0.65
1:A:976:GLN:NE2	5:A:1203:HOH:O	2.29	0.65
1:D:861:LEU:HD13	1:D:861:LEU:H	1.61	0.64
1:C:983:GLY:HA2	1:C:986:ARG:NH2	2.13	0.64
1:B:905:TRP:HD1	1:B:947:MET:HE1	1.63	0.64
1:B:749:GLU:O	1:B:751:THR:HG22	1.98	0.63
1:A:730:LEU:HD13	1:A:739:LYS:HE3	1.80	0.63
1:B:754:LYS:HE3	1:B:758:GLU:HG3	1.81	0.63
1:C:782:LEU:HG	1:C:782:LEU:O	1.98	0.63
1:C:776:ARG:NE	5:C:1401:HOH:O	2.32	0.62
2:D:1101:ANP:O2B	2:D:1101:ANP:O1G	2.17	0.62
1:D:905:TRP:HD1	1:D:947:MET:HE1	1.65	0.62
1:A:944:TYR:CZ	1:A:948:ARG:HD3	2.35	0.61
1:C:750:ALA:O	1:C:751:THR:HG22	1.95	0.61
1:A:762:GLU:HG2	1:A:860:LYS:HE3	1.83	0.61
1:C:941:ILE:O	1:C:945:MET:HG2	2.01	0.60
1:B:867:LYS:H	1:B:867:LYS:HD2	1.68	0.59
1:C:793:MET:HE1	1:C:852:LYS:HD3	1.85	0.59
1:A:905:TRP:CD1	1:A:947:MET:HE1	2.38	0.58
1:B:754:LYS:HE3	1:B:758:GLU:CG	2.34	0.58
1:B:865:GLU:HB3	1:B:867:LYS:HD3	1.85	0.58
1:D:750:ALA:HA	1:D:784:SER:O	2.03	0.58
1:A:793:MET:HE2	1:A:846:LYS:HA	1.86	0.57
1:C:812:GLN:HG2	1:C:975:PRO:HG3	1.87	0.57
1:B:867:LYS:HD2	1:B:867:LYS:N	2.19	0.56
1:D:995:SER:O	1:D:999:ARG:HG3	2.06	0.56
1:B:989:LEU:HD12	1:B:989:LEU:N	2.19	0.56
1:C:905:TRP:HD1	1:C:947:MET:HE1	1.71	0.56
1:D:762:GLU:HG3	1:D:861:LEU:HD12	1.87	0.56
1:C:918:ILE:HG21	1:C:926:ILE:HD11	1.88	0.56
1:B:809:ILE:CA	1:B:988:HIS:CE1	2.70	0.56
1:D:762:GLU:HG3	1:D:861:LEU:CD1	2.36	0.56
1:A:805:HIS:O	1:A:809:ILE:HG13	2.05	0.56
1:C:909:THR:CB	1:C:912:SER:HB2	2.35	0.56
1:C:962:ARG:HA	1:C:965:ILE:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:745:LYS:NZ	2:A:1101:ANP:O2A	2.39	0.55
1:A:998:TYR:HE2	5:A:1248:HOH:O	1.88	0.55
1:C:991:SER:HB2	1:C:994:ASP:H	1.72	0.55
1:C:732:ILE:HG12	1:C:739:LYS:HG2	1.88	0.55
1:A:892:THR:H	1:A:895:SER:HB3	1.72	0.54
1:B:868:GLU:HB2	1:B:876:VAL:HG23	1.89	0.54
1:B:748:ARG:HG2	1:B:748:ARG:NH2	2.23	0.54
1:B:1010:VAL:HG22	1:B:1015:GLU:HG3	1.88	0.54
2:D:1101:ANP:H8	5:D:1232:HOH:O	2.07	0.54
1:A:749:GLU:CD	1:A:749:GLU:H	2.15	0.54
1:B:868:GLU:HG3	1:B:876:VAL:CG2	2.38	0.54
1:C:836:ARG:HD3	1:C:859:ALA:HB2	1.90	0.54
1:A:944:TYR:O	1:A:948:ARG:HG2	2.08	0.54
1:B:793:MET:HE1	1:B:852:LYS:HD3	1.89	0.53
1:C:941:ILE:H	1:C:941:ILE:HD12	1.72	0.53
1:A:712:PHE:O	1:A:713:LYS:HD2	2.09	0.53
1:D:984:ASP:HA	1:D:987:MET:HE2	1.89	0.53
1:D:750:ALA:CA	1:D:784:SER:O	2.57	0.53
1:D:750:ALA:HB1	1:D:784:SER:O	2.09	0.53
1:D:705:ARG:NH2	1:D:711:GLU:OE1	2.42	0.52
1:D:882:ALA:HA	1:D:898:TRP:CD2	2.43	0.52
1:A:876:VAL:O	1:A:878:ILE:N	2.42	0.52
1:B:868:GLU:HG3	1:B:876:VAL:HG23	1.91	0.52
1:B:949:LYS:O	1:B:952:MET:HG3	2.09	0.52
1:C:722:ALA:O	1:C:748:ARG:HD2	2.09	0.52
1:B:867:LYS:CD	1:B:867:LYS:N	2.71	0.52
1:A:926:ILE:O	1:A:931:GLU:HG2	2.10	0.52
1:B:1001:LEU:HD11	1:C:742:VAL:HG12	1.92	0.52
1:B:836:ARG:HD3	1:B:891:TYR:CG	2.45	0.51
1:B:989:LEU:HD13	1:B:989:LEU:O	2.11	0.51
1:C:905:TRP:CZ3	1:C:912:SER:O	2.61	0.51
1:A:841:ARG:HH12	1:A:877:PRO:HB3	1.75	0.51
1:B:1017:LEU:HD12	5:B:1239:HOH:O	2.10	0.51
1:D:920:ALA:HA	1:D:923:ILE:HG12	1.92	0.50
1:C:974:ASP:OD2	1:C:977:ARG:NH1	2.44	0.50
1:B:836:ARG:HA	5:B:1228:HOH:O	2.11	0.50
1:D:805:HIS:O	1:D:809:ILE:HG13	2.12	0.50
1:D:985:GLU:HG2	1:D:986:ARG:HG2	1.93	0.50
1:C:782:LEU:HD23	1:C:782:LEU:N	2.26	0.50
2:D:1101:ANP:C2'	5:D:1209:HOH:O	2.60	0.50
1:C:747:LEU:HB2	1:C:786:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1018:ILE:HD13	1:B:1019:PRO:HD2	1.94	0.49
1:A:984:ASP:HA	1:A:987:MET:HE2	1.95	0.49
1:D:750:ALA:CB	1:D:784:SER:O	2.60	0.49
1:C:821:ILE:HG23	1:C:853:ILE:HD11	1.95	0.49
1:A:783:THR:HG21	1:A:787:GLN:HG3	1.95	0.48
1:A:793:MET:CE	1:A:846:LYS:HA	2.43	0.48
1:C:751:THR:N	5:C:1402:HOH:O	2.39	0.48
1:C:983:GLY:HA2	1:C:986:ARG:HH21	1.77	0.48
1:C:794:PRO:HD2	5:C:1407:HOH:O	2.14	0.48
1:C:922[A]:GLU:O	1:C:926:ILE:HG13	2.12	0.48
1:D:769:VAL:HG11	1:D:856:PHE:CZ	2.48	0.48
1:A:837:ASP:OD1	1:A:877:PRO:HG3	2.13	0.48
1:A:922[A]:GLU:O	1:A:926:ILE:HG23	2.13	0.48
1:A:783:THR:HG1	1:A:785:THR:H	1.57	0.47
1:A:883:LEU:HD21	1:A:928:GLU:HG3	1.96	0.47
1:C:730:LEU:HD13	1:C:739:LYS:HB3	1.94	0.47
1:A:810:GLY:HA2	1:A:987:MET:HE3	1.94	0.47
1:A:791:GLN:HG3	5:A:1202:HOH:O	2.13	0.47
1:B:875:LYS:O	1:B:875:LYS:HG2	2.14	0.47
1:B:929:LYS:O	1:B:929:LYS:HG3	2.13	0.47
1:D:812:GLN:HG3	1:D:816:ASN:HD22	1.80	0.47
1:A:748:ARG:NE	1:A:875:LYS:HZ2	2.13	0.47
1:B:749:GLU:HB3	1:B:750:ALA:H	1.60	0.47
1:C:926:ILE:HG22	1:C:931:GLU:HB3	1.95	0.47
1:D:857:GLY:HA2	1:D:860:LYS:HG3	1.96	0.47
1:C:813:TYR:OH	1:C:990:PRO:HD3	2.15	0.47
1:A:981:ILE:HG21	1:A:987:MET:HE1	1.97	0.47
1:C:775:CYS:SG	1:C:790:MET:HE1	2.55	0.47
1:D:900:TYR:O	1:D:904:VAL:HG23	2.13	0.47
1:A:823:LYS:HA	1:A:965:ILE:HD11	1.97	0.47
1:A:1012:ASP:OD1	1:A:1013:ALA:N	2.48	0.47
1:B:780:ILE:HD11	1:B:782:LEU:HD21	1.97	0.46
1:C:721:GLY:O	1:C:748:ARG:CZ	2.64	0.46
1:B:808:ASN:O	1:B:988:HIS:NE2	2.49	0.46
1:D:937:PRO:HD2	5:D:1210:HOH:O	2.14	0.46
1:D:986:ARG:NH1	1:D:986:ARG:HB3	2.31	0.46
1:A:809:ILE:HB	1:A:910:PHE:HE1	1.80	0.46
1:B:850:HIS:HE1	1:B:1005:GLU:OE2	1.98	0.46
1:B:926:ILE:HG23	1:B:931:GLU:HB2	1.97	0.46
1:D:705:ARG:HG2	1:D:707:LEU:HD22	1.98	0.45
1:B:945:MET:O	1:B:949:LYS:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:915:TYR:HB3	1:D:918:ILE:HD12	1.99	0.45
1:B:748:ARG:HG2	1:B:748:ARG:HH21	1.79	0.45
1:D:732:ILE:HG22	5:D:1218:HOH:O	2.15	0.45
1:D:860:LYS:HB3	1:D:860:LYS:HE3	1.55	0.45
1:B:742:VAL:HG12	1:C:1001:LEU:HD22	1.98	0.45
1:B:810:GLY:N	1:B:988:HIS:ND1	2.52	0.45
1:D:945:MET:HE3	1:D:945:MET:HB3	1.79	0.45
1:A:829:GLU:HG3	1:A:893:HIS:CG	2.52	0.45
1:B:960:LYS:HB3	5:B:1229:HOH:O	2.17	0.45
1:D:757:LYS:HD3	1:D:761:ASP:OD2	2.17	0.45
1:B:793:MET:HG3	1:B:844:LEU:HD13	1.98	0.45
1:A:714:LYS:HD2	1:A:727:TYR:CG	2.52	0.45
1:A:755:ALA:O	1:A:759:ILE:HD12	2.16	0.45
1:B:850:HIS:CE1	1:B:1005:GLU:OE2	2.70	0.45
1:C:841:ARG:NH1	1:C:877:PRO:HB3	2.30	0.45
1:B:1018:ILE:HB	5:B:1239:HOH:O	2.16	0.45
1:B:1017:LEU:HG	1:B:1017:LEU:O	2.16	0.44
1:C:757:LYS:HD2	1:C:757:LYS:HA	1.61	0.44
1:D:894:GLN:OE1	1:D:960:LYS:NZ	2.48	0.44
1:A:709:GLU:OE1	1:A:783:THR:HB	2.17	0.44
1:C:715:ILE:HD12	1:C:730:LEU:HG	2.00	0.44
1:C:748:ARG:C	1:C:749:GLU:HG3	2.42	0.44
1:A:750:ALA:HB2	1:A:862:LEU:HD23	1.99	0.43
1:D:824:GLY:HA3	1:D:853:ILE:HD12	2.00	0.43
1:B:749:GLU:O	1:B:751:THR:N	2.47	0.43
1:C:756:ASN:HB3	1:C:782:LEU:HD12	1.99	0.43
1:B:772:PRO:HA	1:B:1005:GLU:OE1	2.19	0.43
1:C:811:SER:HB2	1:C:975:PRO:HB2	2.01	0.43
1:C:724:GLY:H	1:C:748:ARG:HG2	1.83	0.43
1:C:876:VAL:HG13	1:C:878:ILE:HG12	2.01	0.43
1:A:802:VAL:HA	1:A:809:ILE:HD11	2.00	0.43
1:D:946:ILE:HD11	1:D:967:GLU:HG2	2.00	0.42
1:C:960:LYS:HD2	1:C:960:LYS:HA	1.71	0.42
1:D:782:LEU:HD22	1:D:786:VAL:HG22	2.01	0.42
1:B:987:MET:HE2	1:B:987:MET:HB2	1.93	0.42
1:D:835:HIS:CD2	1:D:856:PHE:HB3	2.54	0.42
1:B:708:LYS:H	1:B:708:LYS:HG2	1.70	0.42
1:C:905:TRP:HB2	1:C:947:MET:HE3	2.01	0.42
1:B:926:ILE:CG2	1:B:931:GLU:HB2	2.49	0.42
1:C:949:LYS:HA	1:C:952:MET:HG3	2.01	0.42
1:B:747:LEU:HD22	1:B:862:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:918:ILE:N	1:C:918:ILE:HD13	2.33	0.42
1:B:757:LYS:HG2	1:B:761:ASP:OD2	2.19	0.42
1:C:985:GLU:HB2	1:C:986:ARG:HD3	2.01	0.42
1:B:713:LYS:HA	1:B:713:LYS:HD3	1.83	0.42
1:A:816:ASN:O	1:A:820:GLN:HG3	2.19	0.42
1:A:881:MET:HE2	1:A:886:ILE:HG13	2.01	0.41
1:B:882:ALA:HA	1:B:898:TRP:CD2	2.55	0.41
1:C:850:HIS:ND1	1:C:1003:ASP:OD2	2.53	0.41
1:C:983:GLY:C	1:C:987:MET:HE2	2.45	0.41
1:A:887:LEU:HD23	1:A:888:HIS:CE1	2.55	0.41
1:A:944:TYR:CE2	1:A:948:ARG:HD3	2.54	0.41
1:B:823:LYS:HA	1:B:965:ILE:HD11	2.02	0.41
1:C:799:LEU:O	1:C:803:ARG:HG3	2.20	0.41
1:C:922[B]:GLU:O	1:C:926:ILE:HG13	2.19	0.41
1:A:953:ILE:O	5:A:1201:HOH:O	2.22	0.41
1:B:701:GLN:N	5:B:1210:HOH:O	2.54	0.41
1:A:938:ILE:HD12	1:A:981:ILE:HD11	2.01	0.41
1:D:935:GLN:HB2	1:D:944:TYR:CE2	2.56	0.41
1:D:879:LYS:HD3	1:D:914:PRO:O	2.20	0.40
1:B:954:ASP:OD2	1:B:957:SER:OG	2.39	0.40
1:C:769:VAL:O	1:C:769:VAL:HG23	2.21	0.40
1:A:832:ARG:HE	1:A:832:ARG:HB3	1.61	0.40
1:C:898:TRP:CD1	1:C:898:TRP:C	2.99	0.40
1:B:856:PHE:CD1	1:B:856:PHE:C	2.98	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	292/328 (89%)	282 (97%)	9 (3%)	1 (0%)	36 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	313/328 (95%)	290 (93%)	19 (6%)	4 (1%)	9	14
1	C	296/328 (90%)	286 (97%)	9 (3%)	1 (0%)	36	50
1	D	292/328 (89%)	278 (95%)	14 (5%)	0	100	100
All	All	1193/1312 (91%)	1136 (95%)	51 (4%)	6 (0%)	24	37

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	783	THR
1	B	753	PRO
1	C	751	THR
1	B	750	ALA
1	B	991	SER
1	B	989	LEU

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	264/288 (92%)	262 (99%)	2 (1%)	73	86
1	B	283/288 (98%)	269 (95%)	14 (5%)	22	39
1	C	267/288 (93%)	257 (96%)	10 (4%)	30	51
1	D	266/288 (92%)	259 (97%)	7 (3%)	40	63
All	All	1080/1152 (94%)	1047 (97%)	33 (3%)	35	57

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	748	ARG
1	D	749	GLU
1	D	858	LEU
1	D	860	LYS
1	D	861	LEU

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Mol	Chain	Res	Type
1	D	945	MET
1	D	970	LYS
1	A	739	LYS
1	A	832	ARG
1	B	751	THR
1	B	752	SER
1	B	754	LYS
1	B	862	LEU
1	B	868	GLU
1	B	987	MET
1	B	989	LEU
1	B	1006	ASP
1	B	1009	ASP
1	B	1010	VAL
1	B	1012	ASP
1	B	1017	LEU
1	B	1018	ILE
1	B	1020	GLN
1	C	737	LYS
1	C	745	LYS
1	C	748	ARG
1	C	816	ASN
1	C	875	LYS
1	C	876	VAL
1	C	913	LYS
1	C	918	ILE
1	C	984	ASP
1	C	1006	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	787	GLN
1	D	791	GLN
1	D	982	GLN
1	A	773	HIS
1	A	812	GLN
1	A	816	ASN
1	A	888	HIS
1	B	805	HIS
1	B	849	GLN
1	B	988	HIS

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Mol	Chain	Res	Type
1	C	808	ASN
1	C	935	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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$
2	ANP	D	1101	3	33,33,33	1.18	4 (12%)	45,52,52	0.66	0
2	ANP	B	1101	3	33,33,33	1.16	4 (12%)	45,52,52	0.67	0
4	TQA	C	1301	-	48,48,48	2.68	21 (43%)	64,68,68	2.40	21 (32%)
2	ANP	A	1101	3	33,33,33	1.01	5 (15%)	45,52,52	0.78	2 (4%)

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	ANP	D	1101	3	-	2/18/38/38	0/3/3/3
2	ANP	B	1101	3	-	3/18/38/38	0/3/3/3
4	TQA	C	1301	-	-	4/26/38/38	0/6/6/6
2	ANP	A	1101	3	-	4/18/38/38	0/3/3/3

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1301	TQA	C27-N38	-6.25	1.26	1.37
4	C	1301	TQA	C26-N42	-5.72	1.29	1.38
4	C	1301	TQA	O36-C34	-5.63	1.10	1.23
4	C	1301	TQA	O01-C02	-5.11	1.11	1.23
4	C	1301	TQA	C34-N33	4.98	1.45	1.36
2	D	1101	ANP	PA-O3A	4.74	1.64	1.59
4	C	1301	TQA	C14-N06	4.27	1.42	1.36
4	C	1301	TQA	C30-N31	-4.20	1.25	1.34
4	C	1301	TQA	O15-C14	-3.80	1.14	1.22
4	C	1301	TQA	C39-S40	3.79	1.81	1.75
4	C	1301	TQA	C27-C26	-3.40	1.32	1.38
2	B	1101	ANP	PG-O1G	3.37	1.51	1.46
4	C	1301	TQA	C25-C26	3.37	1.53	1.48
2	B	1101	ANP	PA-O3A	3.33	1.63	1.59
4	C	1301	TQA	C03-C04	-3.28	1.36	1.40
4	C	1301	TQA	C37-C28	-3.17	1.34	1.39
4	C	1301	TQA	C13-C14	3.11	1.53	1.48
2	B	1101	ANP	PB-O1B	3.01	1.50	1.46
4	C	1301	TQA	C32-N31	-2.83	1.29	1.34
2	D	1101	ANP	PG-O1G	2.64	1.50	1.46
2	A	1101	ANP	PG-O1G	2.62	1.50	1.46
2	A	1101	ANP	PA-O3A	2.54	1.62	1.59
4	C	1301	TQA	C39-N38	-2.52	1.30	1.36
2	A	1101	ANP	PB-O1B	2.42	1.49	1.46
2	D	1101	ANP	PB-O1B	2.40	1.49	1.46
4	C	1301	TQA	C43-C25	-2.40	1.35	1.39
2	B	1101	ANP	PG-N3B	2.39	1.69	1.63
4	C	1301	TQA	C07-N06	-2.35	1.43	1.46
2	A	1101	ANP	PG-N3B	2.29	1.69	1.63
2	D	1101	ANP	PG-N3B	2.21	1.69	1.63
4	C	1301	TQA	C03-C02	2.13	1.54	1.50
4	C	1301	TQA	C05-N06	2.07	1.50	1.46
4	C	1301	TQA	C05-C04	-2.07	1.47	1.51
2	A	1101	ANP	PB-N3B	2.02	1.68	1.63

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1301	TQA	C35-C34-N33	8.36	127.52	114.95
4	C	1301	TQA	C08-C07-N06	7.60	105.99	102.42
4	C	1301	TQA	O36-C34-N33	-5.33	115.75	123.06
4	C	1301	TQA	S40-C39-N38	4.31	128.99	119.66
4	C	1301	TQA	C30-N31-C32	4.28	123.33	117.21
4	C	1301	TQA	C04-C05-N06	-3.81	106.94	113.54
4	C	1301	TQA	C24-C25-C26	3.78	126.94	120.74
4	C	1301	TQA	C43-C25-C26	-3.58	113.22	120.51
4	C	1301	TQA	C29-C30-N31	-3.51	119.67	123.97
4	C	1301	TQA	C17-C18-C19	3.34	124.36	120.24
4	C	1301	TQA	C05-C04-C03	-3.12	115.81	122.03
4	C	1301	TQA	O36-C34-C35	-3.01	116.69	122.05
4	C	1301	TQA	C27-C26-N42	-2.95	105.96	109.51
4	C	1301	TQA	C25-C26-C27	2.77	134.49	130.43
4	C	1301	TQA	C18-C17-C16	-2.76	116.84	120.24
2	A	1101	ANP	O2B-PB-O1B	-2.62	104.24	109.87
4	C	1301	TQA	C16-C04-C03	2.48	121.48	118.45
2	A	1101	ANP	O3G-PG-O1G	-2.38	107.47	113.45
4	C	1301	TQA	C03-C02-N20	2.38	120.96	116.03
4	C	1301	TQA	C23-C22-C21	-2.32	117.06	119.73
4	C	1301	TQA	C32-N33-C34	2.22	130.42	128.16
4	C	1301	TQA	C28-C27-C26	-2.19	129.28	133.06
4	C	1301	TQA	O01-C02-N20	-2.09	118.45	123.75

There are no chirality outliers.

All (13) torsion outliers are listed below:

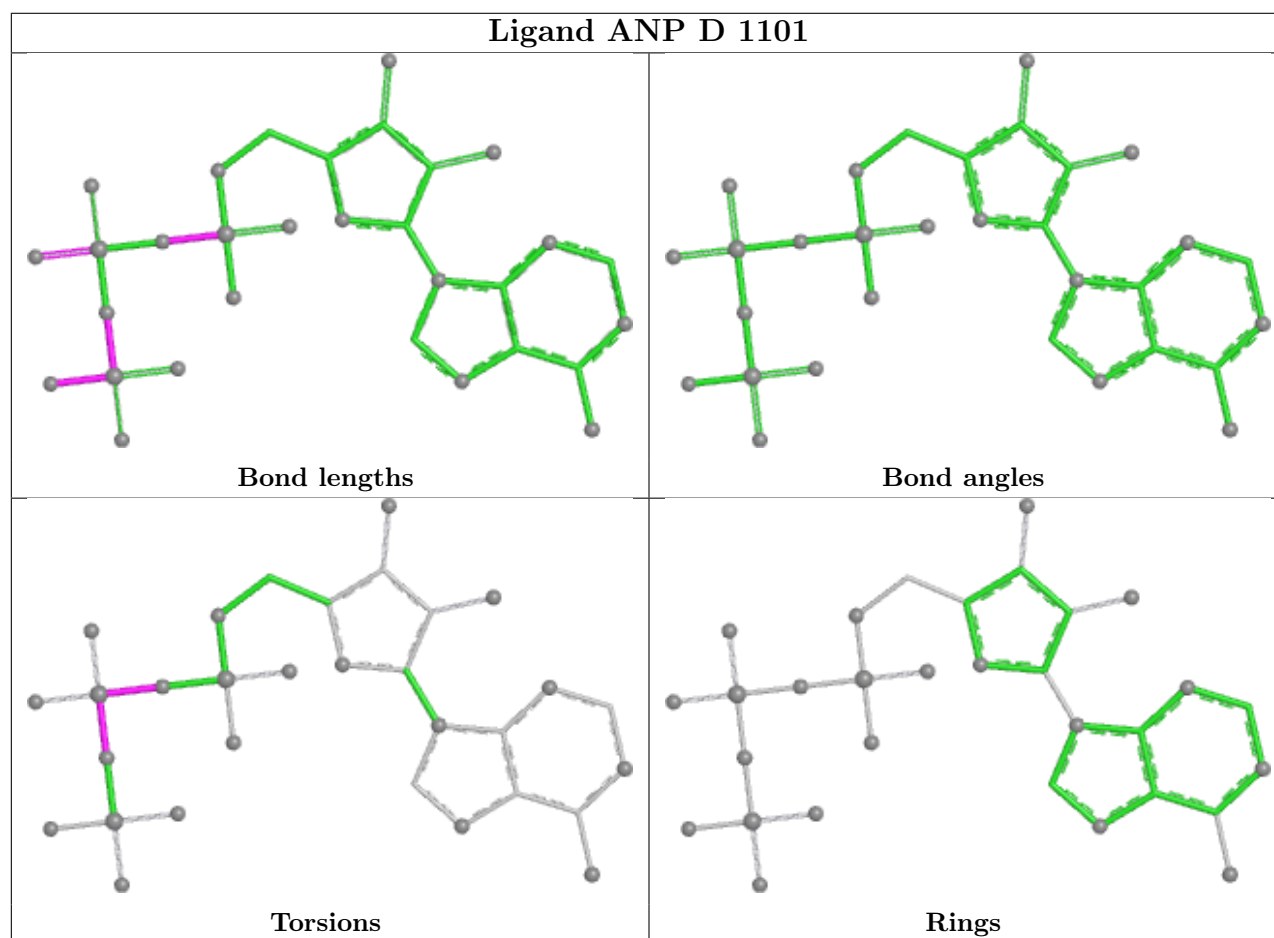
Mol	Chain	Res	Type	Atoms
2	D	1101	ANP	PG-N3B-PB-O3A
2	D	1101	ANP	PA-O3A-PB-O2B
2	B	1101	ANP	PG-N3B-PB-O1B
2	B	1101	ANP	PA-O3A-PB-O2B
4	C	1301	TQA	N38-C39-S40-C41
4	C	1301	TQA	N42-C39-S40-C41
4	C	1301	TQA	C35-C34-N33-C32
4	C	1301	TQA	O36-C34-N33-C32
2	A	1101	ANP	C5'-O5'-PA-O1A
2	A	1101	ANP	C5'-O5'-PA-O2A
2	A	1101	ANP	C5'-O5'-PA-O3A
2	A	1101	ANP	PB-O3A-PA-O2A
2	B	1101	ANP	PA-O3A-PB-O1B

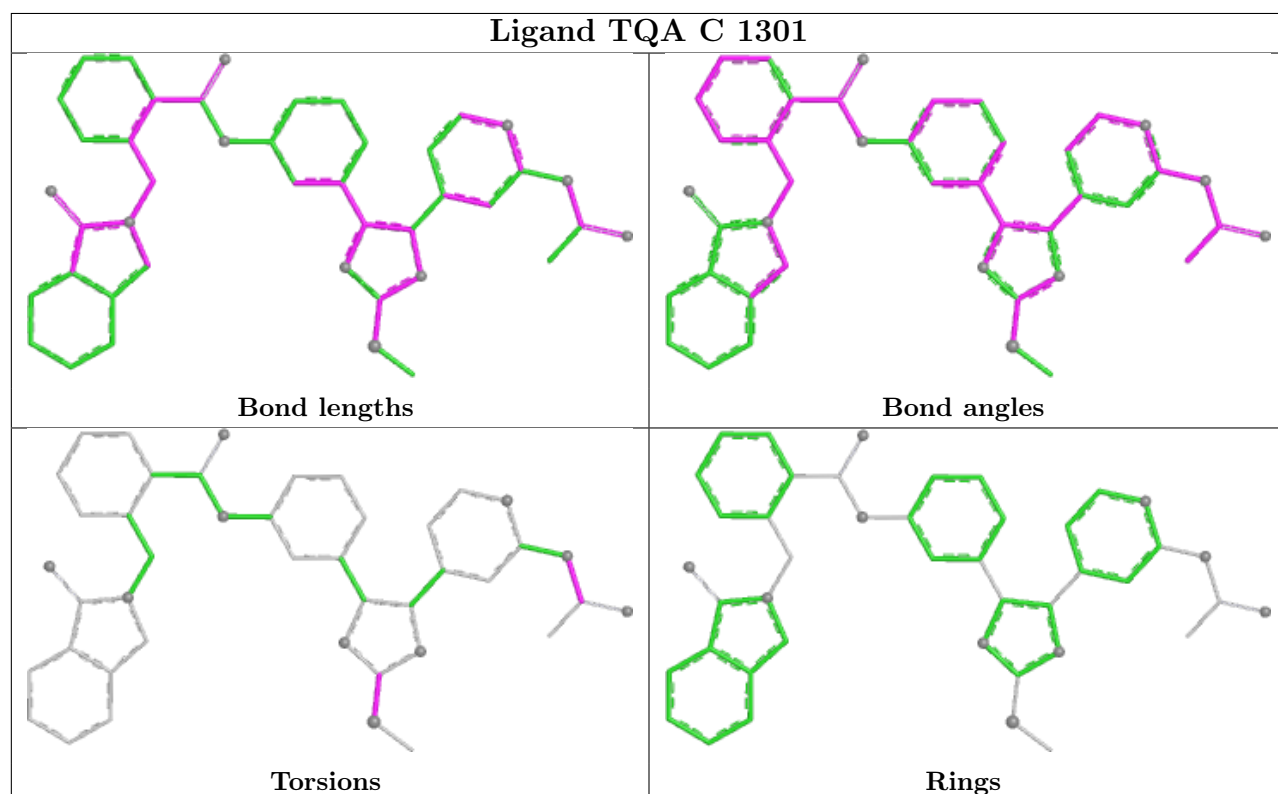
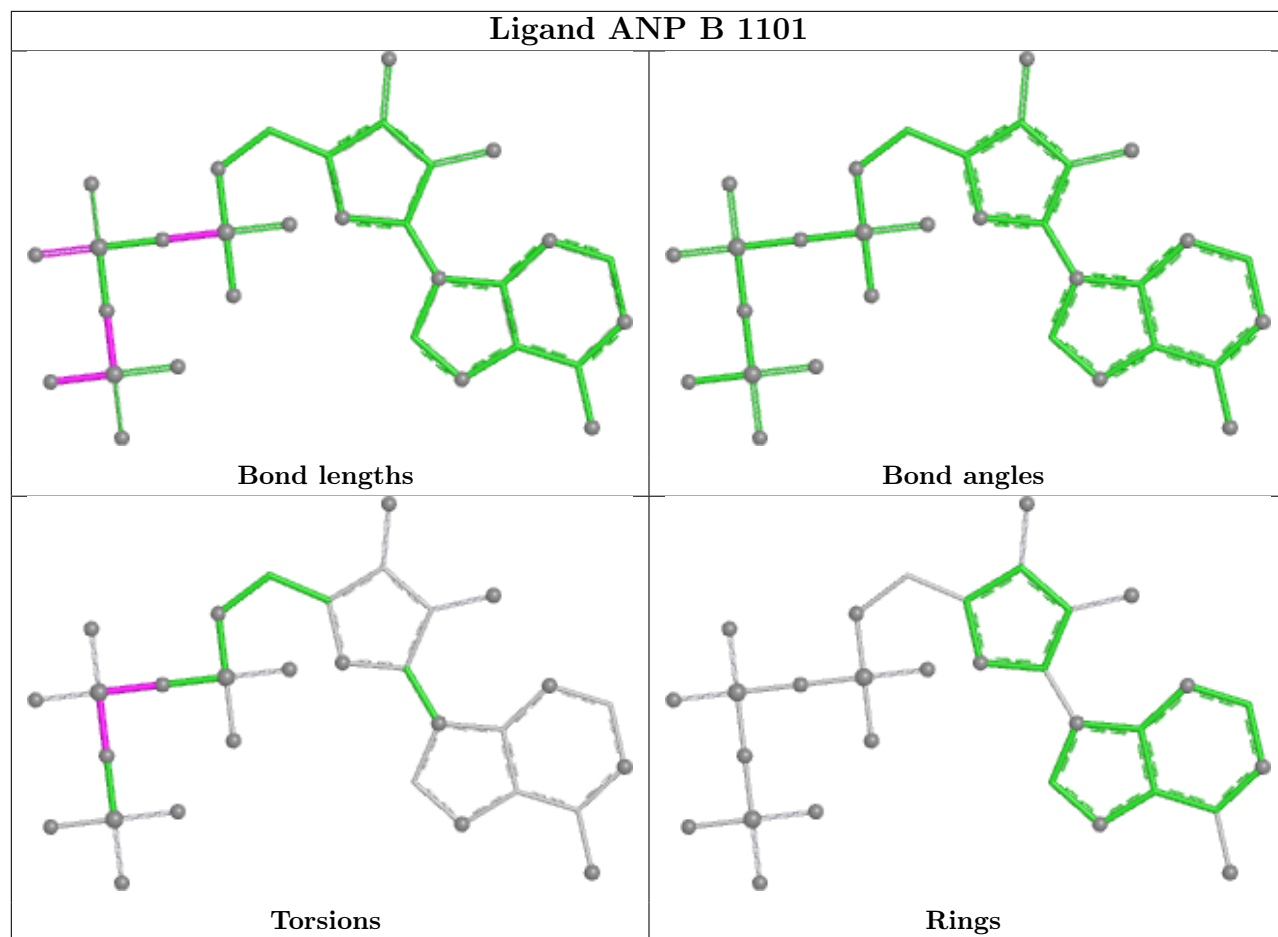
There are no ring outliers.

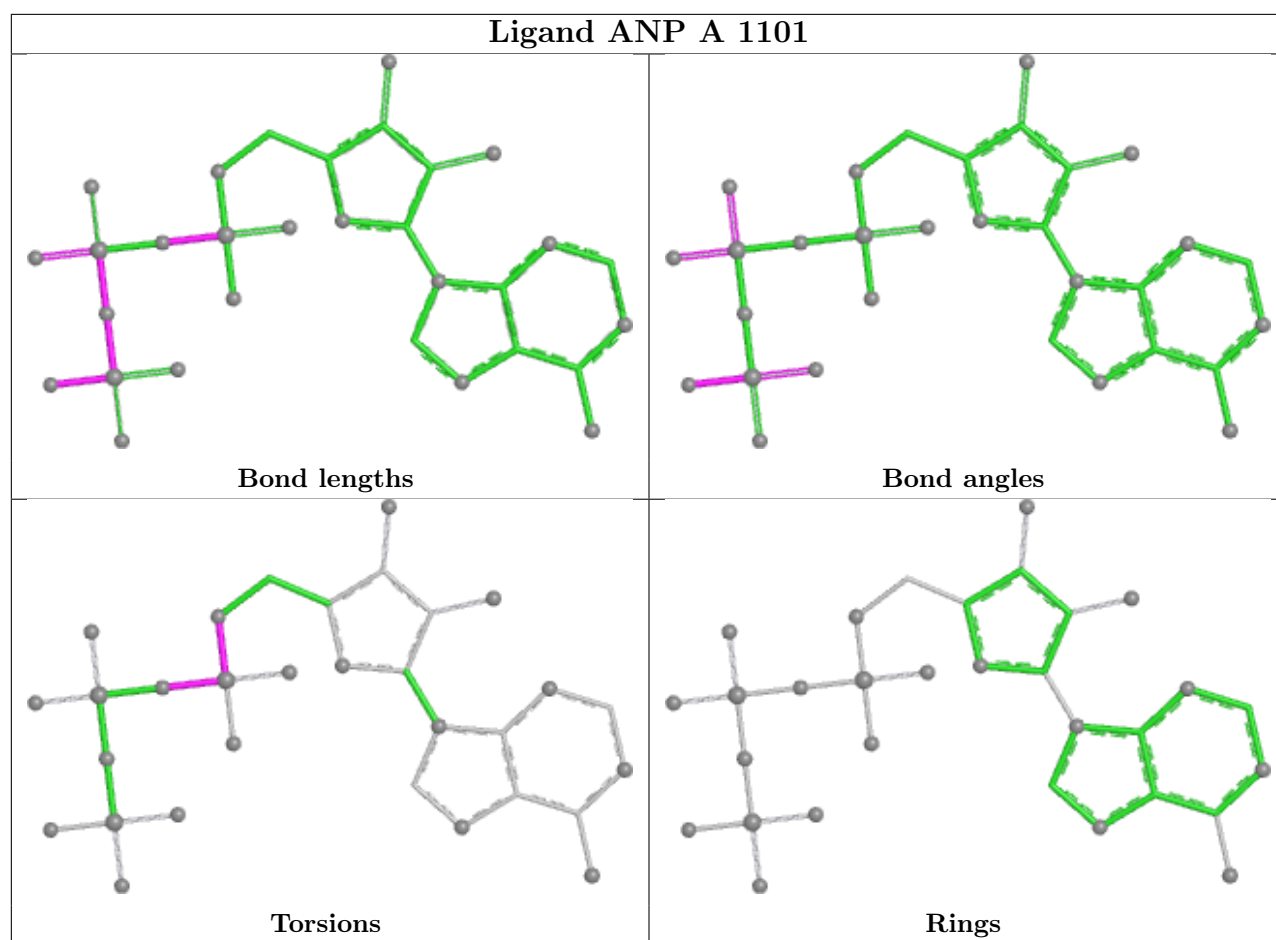
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1101	ANP	5	0
2	A	1101	ANP	1	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	297/328 (90%)	0.74	36 (12%) 8 6	13, 30, 59, 95	1 (0%)
1	B	316/328 (96%)	0.69	44 (13%) 6 5	10, 26, 65, 89	1 (0%)
1	C	299/328 (91%)	0.76	34 (11%) 10 7	11, 29, 64, 80	1 (0%)
1	D	297/328 (90%)	0.50	26 (8%) 15 12	9, 26, 59, 82	1 (0%)
All	All	1209/1312 (92%)	0.67	140 (11%) 9 7	9, 28, 62, 95	4 (0%)

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	784	SER	6.3
1	C	723	PHE	5.9
1	B	988	HIS	5.6
1	B	752	SER	5.5
1	B	1009	ASP	5.5
1	A	751	THR	5.4
1	B	750	ALA	5.3
1	B	1011	VAL	5.3
1	B	753	PRO	5.2
1	B	992	PRO	5.2
1	B	864	ALA	4.9
1	C	982	GLN	4.8
1	C	751	THR	4.6
1	B	989	LEU	4.5
1	A	750	ALA	4.5
1	A	875	LYS	4.4
1	C	988	HIS	4.4
1	C	859	ALA	4.4
1	C	722	ALA	4.3
1	A	863	GLY	4.0
1	B	889	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	751	THR	3.7
1	D	982	GLN	3.7
1	B	737	LYS	3.6
1	D	750	ALA	3.5
1	C	983	GLY	3.5
1	D	748	ARG	3.5
1	B	758	GLU	3.5
1	C	750	ALA	3.5
1	B	865	GLU	3.4
1	B	866	GLU	3.4
1	B	1013	ALA	3.4
1	C	783	THR	3.3
1	C	720	SER	3.3
1	B	1014	ASP	3.3
1	B	784	SER	3.3
1	B	749	GLU	3.3
1	A	1013	ALA	3.3
1	D	723	PHE	3.2
1	D	755	ALA	3.2
1	B	1017	LEU	3.2
1	D	876	VAL	3.2
1	C	785	THR	3.2
1	D	861	LEU	3.2
1	A	860	LYS	3.2
1	B	990	PRO	3.2
1	B	1019	PRO	3.2
1	C	782	LEU	3.2
1	A	922[A]	GLU	3.1
1	D	1012	ASP	3.1
1	B	870	HIS	3.1
1	B	1010	VAL	3.1
1	B	785	THR	3.1
1	D	988	HIS	3.1
1	D	977	ARG	3.1
1	C	918	ILE	3.1
1	A	753	PRO	3.0
1	B	860	LYS	3.0
1	C	912	SER	3.0
1	D	857	GLY	3.0
1	B	993	THR	3.0
1	D	1010	VAL	2.9
1	D	1008	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	752	SER	2.9
1	B	991	SER	2.9
1	A	874	GLY	2.9
1	D	808	ASN	2.9
1	C	876	VAL	2.9
1	A	807	ASP	2.9
1	C	1008	ASP	2.8
1	C	749	GLU	2.8
1	C	977	ARG	2.8
1	A	859	ALA	2.8
1	D	749	GLU	2.7
1	C	701	GLN	2.7
1	B	757	LYS	2.7
1	A	755	ALA	2.7
1	B	701	GLN	2.7
1	C	808	ASN	2.6
1	A	716	LYS	2.6
1	B	754	LYS	2.6
1	A	702	ALA	2.6
1	A	1012	ASP	2.6
1	C	1014	ASP	2.6
1	A	783	THR	2.6
1	A	862	LEU	2.6
1	A	982	GLN	2.6
1	C	784	SER	2.5
1	C	1007	MET	2.5
1	B	1015	GLU	2.5
1	C	1011	VAL	2.5
1	A	985	GLU	2.5
1	C	1012	ASP	2.5
1	D	856	PHE	2.5
1	A	970	LYS	2.5
1	B	1020	GLN	2.5
1	D	860	LYS	2.4
1	D	807	ASP	2.4
1	B	869	TYR	2.4
1	C	1010	VAL	2.4
1	D	985	GLU	2.4
1	D	976	GLN	2.3
1	B	1012	ASP	2.3
1	D	987	MET	2.3
1	B	986	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	1006	ASP	2.3
1	A	707	LEU	2.3
1	C	989	LEU	2.3
1	D	986	ARG	2.3
1	A	889	ARG	2.3
1	A	920	ALA	2.2
1	A	886	ILE	2.2
1	B	985	GLU	2.2
1	A	748	ARG	2.2
1	C	986	ARG	2.2
1	C	875	LYS	2.2
1	D	1009	ASP	2.2
1	B	868	GLU	2.2
1	B	977	ARG	2.2
1	A	723	PHE	2.2
1	A	998	TYR	2.1
1	B	762	GLU	2.1
1	A	921	SER	2.1
1	A	1011	VAL	2.1
1	D	783	THR	2.1
1	C	832	ARG	2.1
1	D	762	GLU	2.1
1	C	921	SER	2.1
1	A	808	ASN	2.1
1	A	986	ARG	2.1
1	B	970	LYS	2.1
1	D	858	LEU	2.0
1	A	953	ILE	2.0
1	B	1018	ILE	2.0
1	A	954	ASP	2.0
1	B	1007	MET	2.0
1	A	988	HIS	2.0
1	B	876	VAL	2.0
1	C	917	GLY	2.0
1	C	987	MET	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

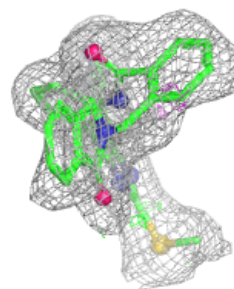
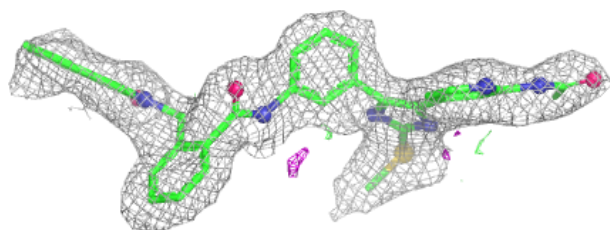
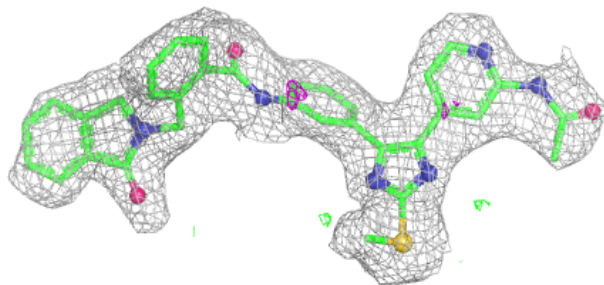
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	B	1102	1/1	0.88	0.09	26,26,26,26	0
4	TQA	C	1301	43/43	0.88	0.11	15,27,38,43	0
2	ANP	A	1101	31/31	0.90	0.10	21,33,42,49	0
2	ANP	D	1101	31/31	0.92	0.10	14,27,37,39	0
3	MG	A	1102	1/1	0.93	0.10	37,37,37,37	0
3	MG	D	1102	1/1	0.94	0.06	24,24,24,24	0
2	ANP	B	1101	31/31	0.94	0.09	18,27,36,45	0

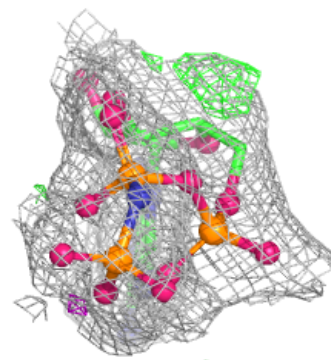
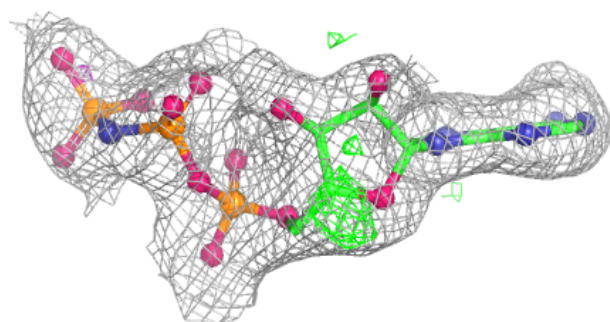
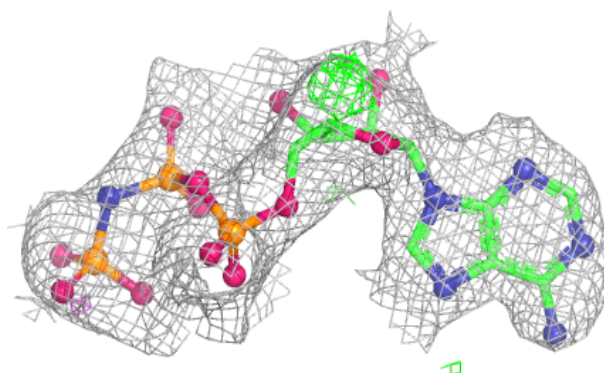
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TQA C 1301:

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

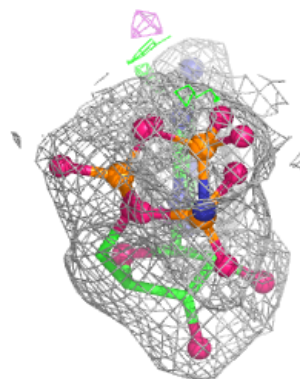
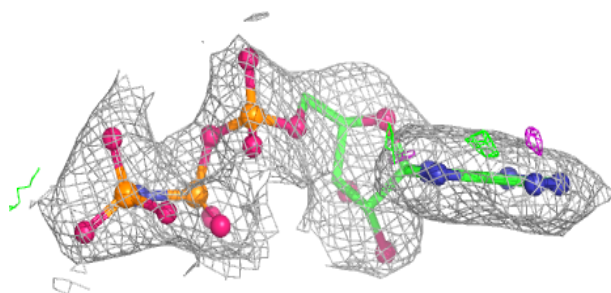
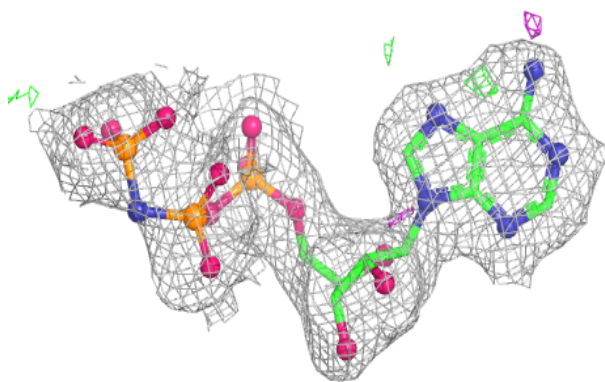
**Electron density around ANP A 1101:**

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

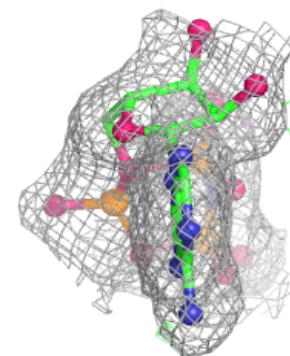
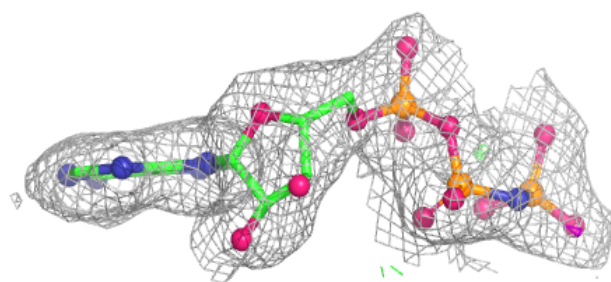
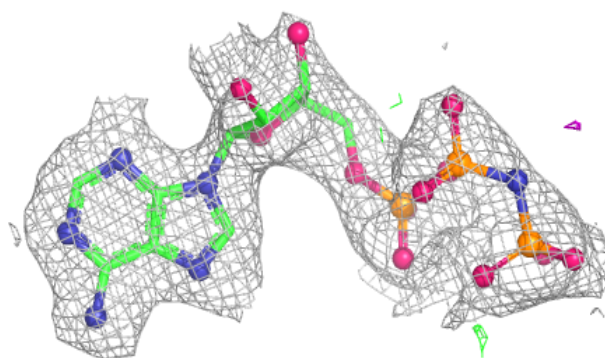


Electron density around ANP D 1101:

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

**Electron density around ANP B 1101:**

$2mF_o-DF_c$ (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.