Full wwPDB X-ray Structure Validation Report (i)

Jan 2, 2024 – 03:49 pm GMT

PDB ID	:	4YDH
Title	:	The structure of human FMNL1 N-terminal domains bound to Cdc42
Authors	:	Kuhn, S.; Anand, K.; Geyer, M.
Deposited on	:	2015-02-22
Resolution	:	3.80 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:

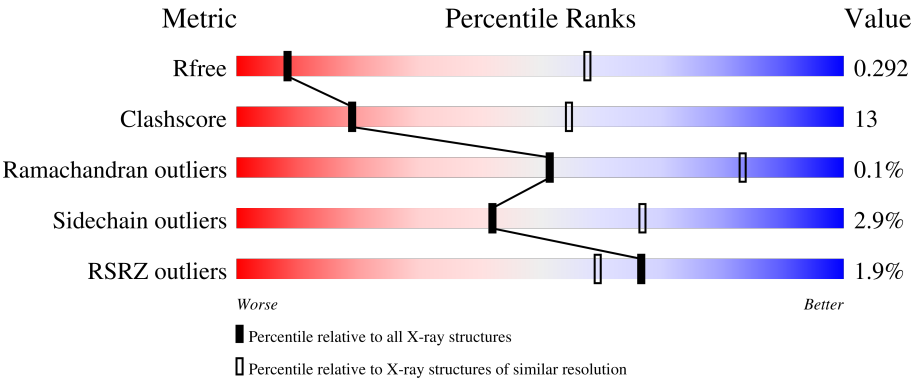
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.80 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	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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	433	% 56% 19% 24%
1	C	433	3% 60% 13% 24%
2	B	181	79% 18%
2	D	181	78% 20%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7564 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 Formin-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	0
			2501	1586	420	477	18			
1	C	328	Total	C	N	O	S	0	0	0
			2363	1495	396	455	17			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP O95466
A	0	ALA	-	expression tag	UNP O95466
A	?	-	ALA	deletion	UNP O95466
A	?	-	SER	deletion	UNP O95466
A	?	-	ASN	deletion	UNP O95466
A	?	-	SER	deletion	UNP O95466
A	?	-	GLU	deletion	UNP O95466
A	?	-	LYS	deletion	UNP O95466
A	?	-	ASN	deletion	UNP O95466
A	?	-	LYS	deletion	UNP O95466
A	?	-	PRO	deletion	UNP O95466
A	?	-	LEU	deletion	UNP O95466
A	?	-	GLU	deletion	UNP O95466
A	?	-	GLN	deletion	UNP O95466
A	?	-	SER	deletion	UNP O95466
A	?	-	VAL	deletion	UNP O95466
A	?	-	GLU	deletion	UNP O95466
A	?	-	ASP	deletion	UNP O95466
A	?	-	LEU	deletion	UNP O95466
A	?	-	SER	deletion	UNP O95466
A	?	-	LYS	deletion	UNP O95466
A	?	-	GLY	deletion	UNP O95466
A	?	-	PRO	deletion	UNP O95466
A	?	-	PRO	deletion	UNP O95466
A	?	-	SER	deletion	UNP O95466

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	SER	deletion	UNP O95466
A	?	-	VAL	deletion	UNP O95466
A	?	-	PRO	deletion	UNP O95466
A	?	-	LYS	deletion	UNP O95466
A	455	ALA	PRO	conflict	UNP O95466
C	-1	GLY	-	expression tag	UNP O95466
C	0	ALA	-	expression tag	UNP O95466
C	?	-	ALA	deletion	UNP O95466
C	?	-	SER	deletion	UNP O95466
C	?	-	ASN	deletion	UNP O95466
C	?	-	SER	deletion	UNP O95466
C	?	-	GLU	deletion	UNP O95466
C	?	-	LYS	deletion	UNP O95466
C	?	-	ASN	deletion	UNP O95466
C	?	-	LYS	deletion	UNP O95466
C	?	-	PRO	deletion	UNP O95466
C	?	-	LEU	deletion	UNP O95466
C	?	-	GLU	deletion	UNP O95466
C	?	-	GLN	deletion	UNP O95466
C	?	-	SER	deletion	UNP O95466
C	?	-	VAL	deletion	UNP O95466
C	?	-	GLU	deletion	UNP O95466
C	?	-	ASP	deletion	UNP O95466
C	?	-	LEU	deletion	UNP O95466
C	?	-	SER	deletion	UNP O95466
C	?	-	LYS	deletion	UNP O95466
C	?	-	GLY	deletion	UNP O95466
C	?	-	PRO	deletion	UNP O95466
C	?	-	PRO	deletion	UNP O95466
C	?	-	SER	deletion	UNP O95466
C	?	-	SER	deletion	UNP O95466
C	?	-	VAL	deletion	UNP O95466
C	?	-	PRO	deletion	UNP O95466
C	?	-	LYS	deletion	UNP O95466
C	455	ALA	PRO	conflict	UNP O95466

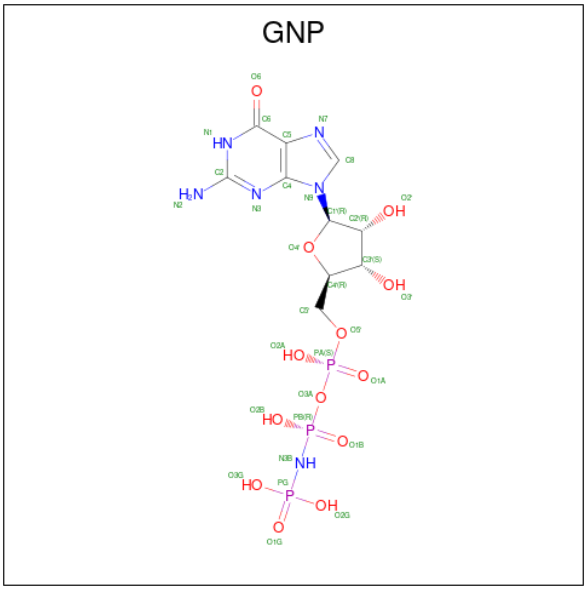
- Molecule 2 is a protein called Cell division control protein 42 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	178	Total	C	N	O	S	0	0	0
			1330	856	206	261	7			
2	D	178	Total	C	N	O	S	0	0	0
			1304	835	203	259	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P60953
B	0	ALA	-	expression tag	UNP P60953
D	-1	GLY	-	expression tag	UNP P60953
D	0	ALA	-	expression tag	UNP P60953

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C N O P 32 10 6 13 3	0	0
3	D	1	Total C N O P 32 10 6 13 3	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

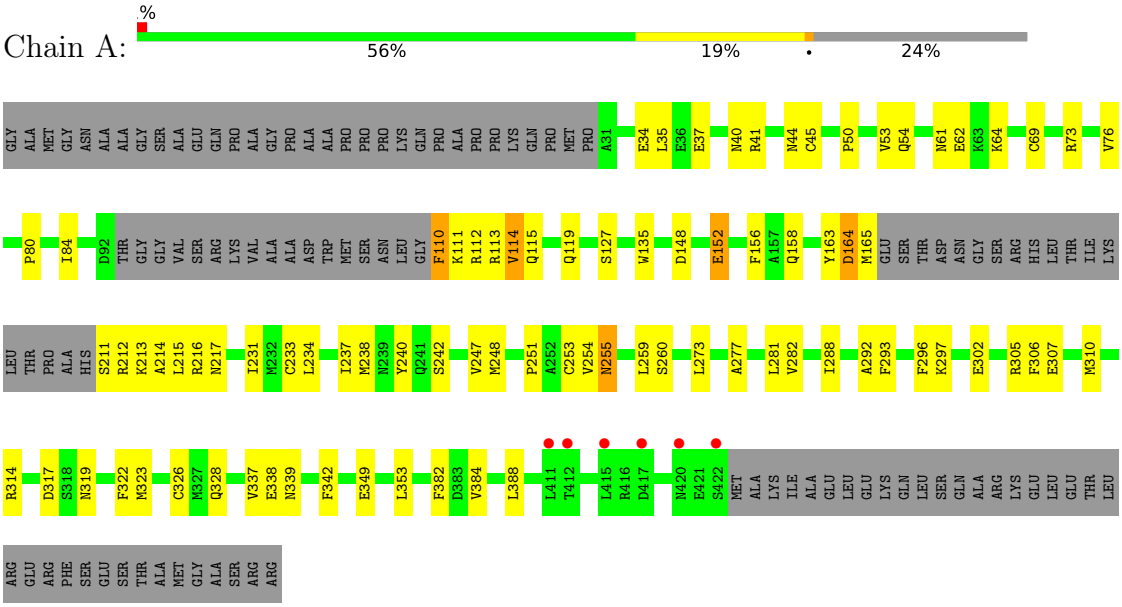
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

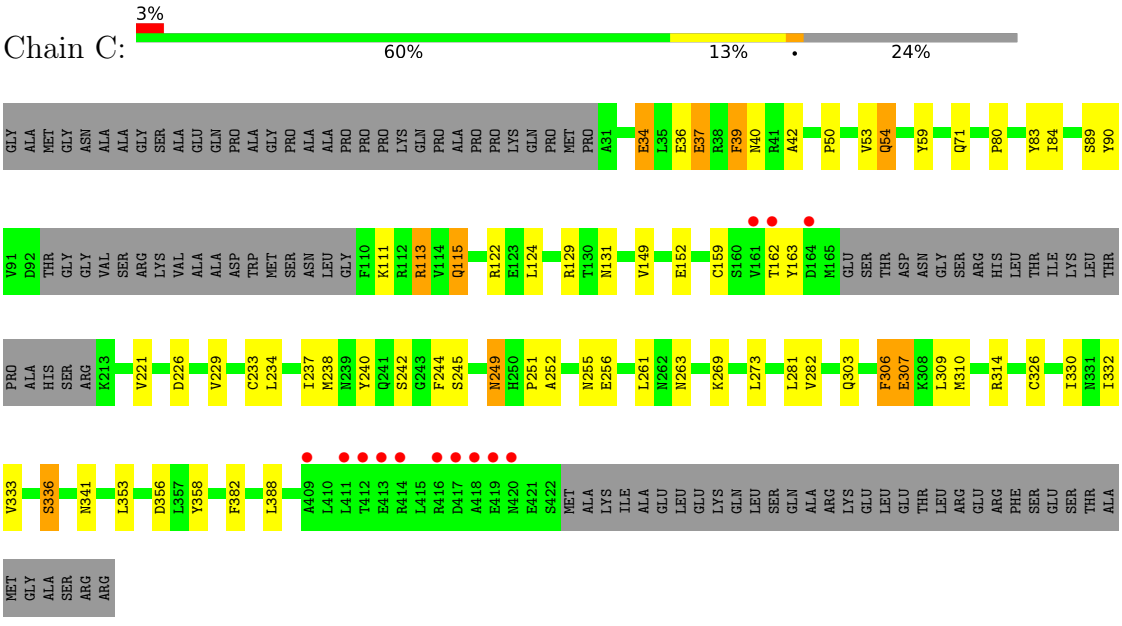
• Molecule 1: Formin-like protein 1

Chain A:



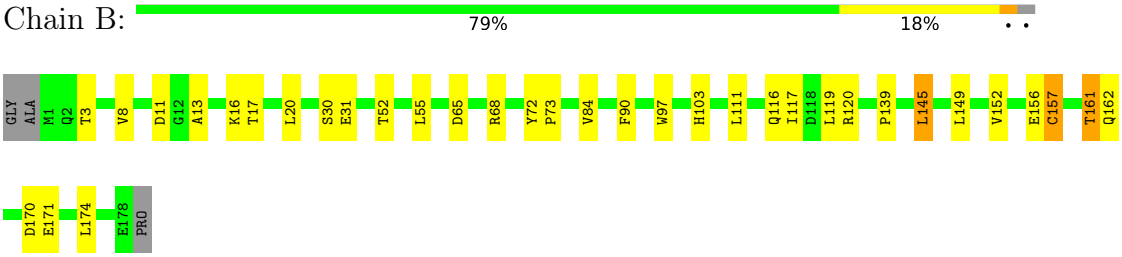
• Molecule 1: Formin-like protein 1

Chain C:



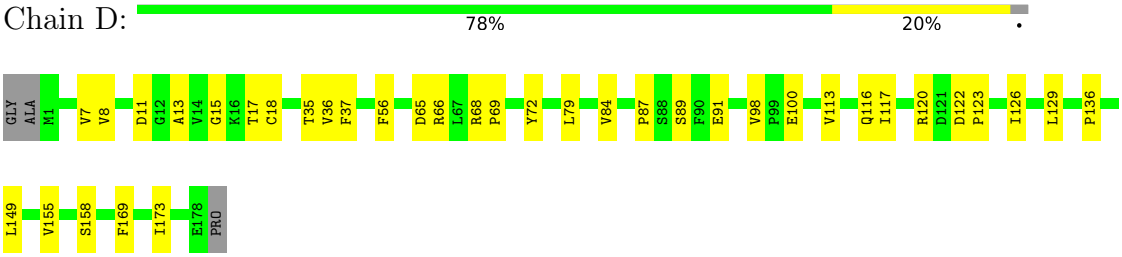
• Molecule 2: Cell division control protein 42 homolog

Chain B:



• Molecule 2: Cell division control protein 42 homolog

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	87.60Å 102.10Å 170.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.70 – 3.80 49.68 – 3.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.70-3.80) 100.0 (49.68-3.80)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.39 (at 3.77Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.208 , 0.281 0.234 , 0.292	Depositor DCC
R_{free} test set	783 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	102.8	Xtriage
Anisotropy	0.455	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 117.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7564	wwPDB-VP
Average B, all atoms (Å^2)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.34	0/2541	0.61	2/3450 (0.1%)
1	C	0.35	0/2404	0.69	4/3287 (0.1%)
2	B	0.34	0/1360	0.59	0/1868
2	D	0.29	0/1334	0.54	0/1839
All	All	0.34	0/7639	0.62	6/10444 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	306	PHE	CB-CA-C	-17.43	75.55	110.40
1	C	306	PHE	N-CA-C	-8.43	88.25	111.00
1	A	164	ASP	N-CA-C	-7.75	90.08	111.00
1	C	307	GLU	CB-CA-C	-6.55	97.30	110.40
1	C	306	PHE	CA-C-N	-5.78	104.48	117.20
1	A	110	PHE	CB-CA-C	-5.18	100.05	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	111	LYS	Peptide

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	2501	0	2299	70	0
1	C	2363	0	2022	64	0
2	B	1330	0	1251	33	0
2	D	1304	0	1201	28	0
3	B	32	0	13	6	0
3	D	32	0	13	4	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
All	All	7564	0	6799	187	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 13.

All (187) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:GLN:HE22	1:A:260:SER:HA	1.09	1.14
1:A:214:ALA:O	1:A:217:ASN:N	1.87	1.07
2:B:145:LEU:HD12	2:B:145:LEU:O	1.54	1.05
1:A:307:GLU:HG2	1:A:307:GLU:O	1.56	1.02
2:B:119:LEU:HD11	3:B:201:GNP:N2	1.75	1.01
1:C:39:PHE:HD2	1:C:39:PHE:C	1.69	0.95
1:A:111:LYS:HG2	1:A:112:ARG:H	1.38	0.89
1:C:89:SER:OG	1:C:113:ARG:NH2	2.06	0.88
1:A:306:PHE:O	1:A:307:GLU:HB3	1.74	0.86
1:C:36:GLU:CD	1:C:36:GLU:C	2.35	0.85
1:C:303:GLN:CD	1:C:307:GLU:OE2	2.12	0.85
2:B:119:LEU:HD11	3:B:201:GNP:HN21	1.45	0.81
1:C:39:PHE:C	1:C:39:PHE:CD2	2.44	0.80
1:C:303:GLN:N	1:C:303:GLN:OE1	2.13	0.79
1:A:111:LYS:HG2	1:A:112:ARG:N	1.97	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:116:GLN:HG2	3:D:201:GNP:C6	2.13	0.78
1:C:306:PHE:O	1:C:353:LEU:CD1	2.32	0.77
1:C:251:PRO:O	1:C:255:ASN:ND2	2.19	0.75
1:A:158:GLN:NE2	1:A:260:SER:HA	1.94	0.74
1:C:39:PHE:HD2	1:C:39:PHE:O	1.70	0.73
1:A:307:GLU:O	1:A:307:GLU:CG	2.35	0.73
1:C:59:TYR:OH	2:D:36:VAL:HG21	1.88	0.72
1:A:111:LYS:NZ	1:A:156:PHE:HZ	1.85	0.72
2:B:65:ASP:OD1	2:B:68:ARG:NH2	2.21	0.71
1:C:34:GLU:C	1:C:34:GLU:OE1	2.30	0.70
1:C:36:GLU:CD	1:C:36:GLU:O	2.29	0.70
2:B:145:LEU:HD11	2:B:149:LEU:HD12	1.74	0.70
1:C:37:GLU:O	1:C:37:GLU:CD	2.30	0.70
1:C:34:GLU:C	1:C:34:GLU:CD	2.51	0.69
1:A:44:ASN:O	1:A:45:CYS:HB3	1.92	0.69
1:C:36:GLU:OE1	1:C:37:GLU:HA	1.93	0.69
2:B:145:LEU:HD12	2:B:145:LEU:C	2.10	0.68
1:C:34:GLU:OE1	1:C:34:GLU:CA	2.38	0.68
1:C:36:GLU:C	1:C:36:GLU:OE1	2.32	0.67
1:A:41:ARG:O	1:A:44:ASN:O	2.13	0.67
1:A:163:TYR:O	1:A:165:MET:N	2.29	0.66
2:B:116:GLN:HE21	3:B:201:GNP:C4	2.08	0.66
1:A:111:LYS:NZ	1:A:156:PHE:CZ	2.64	0.66
1:C:36:GLU:OE1	1:C:37:GLU:N	2.29	0.65
2:B:17:THR:OG1	3:B:201:GNP:O2B	2.13	0.65
1:C:39:PHE:CD2	1:C:39:PHE:O	2.49	0.65
1:A:34:GLU:HG2	1:A:35:LEU:N	2.11	0.64
1:A:110:PHE:CE1	1:A:217:ASN:OD1	2.50	0.64
1:C:245:SER:O	1:C:249:ASN:ND2	2.31	0.63
1:C:37:GLU:CD	1:C:37:GLU:C	2.57	0.63
2:B:11:ASP:OD1	2:B:97:TRP:NE1	2.26	0.63
1:A:110:PHE:HE1	1:A:217:ASN:OD1	1.82	0.62
1:A:212:ARG:HA	1:A:215:LEU:HB2	1.81	0.62
2:B:116:GLN:HG2	3:B:201:GNP:C6	2.30	0.62
2:B:161:THR:O	2:B:162:GLN:C	2.39	0.60
2:D:65:ASP:OD1	2:D:68:ARG:NH2	2.33	0.60
1:A:382:PHE:CE2	1:C:388:LEU:HD11	2.37	0.59
1:A:240:TYR:CZ	1:A:242:SER:HB3	2.37	0.59
2:B:117:ILE:HD11	2:B:156:GLU:HB2	1.85	0.59
1:C:159:CYS:HA	1:C:162:THR:HG22	1.84	0.59
1:A:37:GLU:HG3	1:A:40:ASN:HD22	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:13:ALA:H	3:B:201:GNP:HNB3	1.51	0.59
1:A:214:ALA:O	1:A:215:LEU:C	2.40	0.58
1:C:36:GLU:OE1	1:C:37:GLU:CA	2.50	0.58
1:A:338:GLU:HG2	1:A:339:ASN:H	1.67	0.58
1:A:273:LEU:HD22	1:A:326:CYS:HA	1.86	0.57
1:C:34:GLU:OE1	1:C:34:GLU:HA	2.04	0.57
1:C:306:PHE:O	1:C:353:LEU:HD11	2.04	0.57
1:A:164:ASP:O	1:A:165:MET:HB2	2.05	0.57
1:A:384:VAL:HG12	1:C:341:ASN:OD1	2.05	0.57
2:B:3:THR:HG22	2:B:52:THR:HB	1.88	0.56
2:B:145:LEU:HD11	2:B:149:LEU:CD1	2.36	0.56
2:D:123:PRO:HA	2:D:126:ILE:HD12	1.87	0.55
1:C:303:GLN:OE1	1:C:307:GLU:OE2	2.23	0.55
1:C:273:LEU:HD13	1:C:326:CYS:HA	1.87	0.55
1:A:40:ASN:O	1:A:44:ASN:ND2	2.41	0.54
1:A:337:VAL:HG11	1:A:342:PHE:HD1	1.71	0.54
1:A:277:ALA:O	1:A:281:LEU:HD12	2.07	0.54
1:A:50:PRO:O	1:A:53:VAL:HG12	2.08	0.53
1:A:231:ILE:HD11	1:A:260:SER:HB3	1.90	0.53
1:C:131:ASN:O	2:D:66:ARG:HD2	2.08	0.53
2:D:129:LEU:HD23	2:D:136:PRO:HD3	1.89	0.53
2:D:15:GLY:HA2	3:D:201:GNP:PA	2.49	0.53
1:A:234:LEU:O	1:A:238:MET:HG3	2.08	0.52
2:D:117:ILE:HG13	2:D:158:SER:HB2	1.91	0.52
2:B:84:VAL:HG11	2:B:120:ARG:HH21	1.75	0.52
1:C:50:PRO:HA	1:C:53:VAL:HG12	1.92	0.52
1:A:119:GLN:N	1:A:119:GLN:OE1	2.43	0.51
1:C:84:ILE:HG23	1:C:149:VAL:HG11	1.93	0.51
1:A:114:VAL:O	1:A:115:GLN:C	2.49	0.51
1:A:293:PHE:HA	1:A:296:PHE:HB3	1.91	0.51
2:B:171:GLU:HA	2:B:174:LEU:HD22	1.92	0.51
2:B:171:GLU:HA	2:B:174:LEU:HB2	1.92	0.51
1:C:234:LEU:O	1:C:238:MET:HG3	2.11	0.51
1:C:34:GLU:O	1:C:34:GLU:CG	2.59	0.50
1:C:240:TYR:CZ	1:C:242:SER:HB3	2.47	0.50
1:C:36:GLU:O	1:C:36:GLU:OE2	2.30	0.50
1:A:110:PHE:CD1	1:A:111:LYS:N	2.80	0.50
2:B:20:LEU:HD22	2:B:55:LEU:HD13	1.94	0.50
1:A:349:GLU:O	1:A:353:LEU:HD13	2.12	0.50
1:C:306:PHE:O	1:C:353:LEU:HD12	2.10	0.50
1:C:314:ARG:HA	1:C:358:TYR:CZ	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:GLU:O	1:C:37:GLU:OE1	2.30	0.50
2:D:18:CYS:SG	3:D:201:GNP:H2'	2.53	0.49
1:C:332:ILE:O	1:C:336:SER:HB3	2.12	0.49
1:A:247:VAL:HG13	1:A:253:CYS:SG	2.52	0.49
1:A:148:ASP:O	1:A:152:GLU:HG2	2.12	0.49
1:A:214:ALA:O	1:A:216:ARG:N	2.46	0.48
1:C:53:VAL:HG13	1:C:54:GLN:OE1	2.13	0.48
2:D:122:ASP:O	2:D:126:ILE:HG13	2.14	0.47
2:D:98:VAL:HG21	2:D:149:LEU:HD13	1.95	0.47
1:C:163:TYR:CG	1:C:163:TYR:O	2.68	0.47
2:D:8:VAL:HG22	2:D:79:LEU:HD12	1.96	0.47
1:A:34:GLU:HG2	1:A:35:LEU:H	1.76	0.47
1:A:305:ARG:O	1:A:306:PHE:HB2	2.15	0.47
1:A:255:ASN:OD1	1:A:292:ALA:HA	2.14	0.47
1:C:129:ARG:NH1	2:D:100:GLU:OE2	2.33	0.47
2:B:120:ARG:NH1	2:B:139:PRO:HG3	2.30	0.46
1:A:111:LYS:HZ2	1:A:156:PHE:HZ	1.58	0.46
1:A:319:ASN:OD1	1:A:322:PHE:N	2.40	0.46
1:A:337:VAL:HG11	1:A:342:PHE:CD1	2.50	0.45
1:A:156:PHE:HE1	1:A:214:ALA:HB1	1.80	0.45
2:D:72:TYR:OH	2:D:100:GLU:OE1	2.29	0.45
2:B:116:GLN:HB3	2:B:119:LEU:HD13	1.96	0.45
1:C:115:GLN:HE21	1:C:115:GLN:HB3	1.50	0.45
2:D:13:ALA:H	3:D:201:GNP:HNB3	1.65	0.45
1:A:310:MET:O	1:A:314:ARG:HB2	2.16	0.45
2:B:145:LEU:C	2:B:145:LEU:CD1	2.81	0.45
1:C:37:GLU:O	1:C:37:GLU:OE2	2.34	0.45
1:A:317:ASP:HA	1:A:323:MET:HE1	1.97	0.44
1:C:244:PHE:CZ	1:C:282:VAL:HG11	2.52	0.44
2:D:36:VAL:HG22	2:D:37:PHE:H	1.81	0.44
2:D:36:VAL:CG2	2:D:37:PHE:N	2.80	0.44
1:A:388:LEU:HD11	1:C:382:PHE:CE2	2.52	0.44
1:A:297:LYS:HG3	1:A:302:GLU:HG2	1.99	0.44
2:D:84:VAL:HG11	2:D:120:ARG:HH21	1.82	0.44
1:C:42:ALA:HB1	1:C:71:GLN:HG2	1.99	0.44
2:D:91:GLU:H	2:D:91:GLU:HG2	1.61	0.44
1:A:76:VAL:HG11	1:A:135:TRP:CD1	2.52	0.44
1:A:388:LEU:HD11	1:C:382:PHE:CZ	2.53	0.44
1:A:164:ASP:O	1:A:165:MET:CB	2.66	0.44
1:A:254:VAL:HG11	1:A:288:ILE:CG2	2.48	0.44
1:A:212:ARG:O	1:A:213:LYS:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:170:ASP:O	2:B:174:LEU:HD13	2.18	0.44
2:B:117:ILE:HG12	2:B:157:CYS:O	2.18	0.43
1:C:263:ASN:O	1:C:269:LYS:NZ	2.38	0.43
2:D:169:PHE:O	2:D:173:ILE:HG13	2.18	0.43
2:B:90:PHE:CZ	2:B:145:LEU:HD23	2.53	0.43
1:C:281:LEU:HD23	1:C:281:LEU:O	2.18	0.43
1:A:111:LYS:C	1:A:113:ARG:N	2.71	0.43
2:B:120:ARG:HH12	2:B:139:PRO:HG3	1.84	0.43
1:C:34:GLU:CD	1:C:34:GLU:O	2.57	0.43
1:A:127:SER:HB2	2:B:103:HIS:HE1	1.83	0.43
2:D:69:PRO:HA	2:D:72:TYR:CD2	2.54	0.43
1:C:36:GLU:OE2	1:C:40:ASN:ND2	2.51	0.42
1:C:261:LEU:HD21	1:C:309:LEU:HD13	2.01	0.42
1:A:111:LYS:CG	1:A:112:ARG:H	2.07	0.42
1:C:252:ALA:HA	1:C:255:ASN:HD22	1.83	0.42
2:D:87:PRO:O	2:D:91:GLU:HG2	2.19	0.42
1:A:35:LEU:HA	1:A:35:LEU:HD12	1.57	0.42
1:C:83:TYR:CG	1:C:124:LEU:HD23	2.55	0.42
1:C:221:VAL:HG13	1:C:226:ASP:OD2	2.20	0.42
2:D:122:ASP:HA	2:D:123:PRO:HD2	1.82	0.42
2:B:149:LEU:HD23	2:B:149:LEU:HA	1.83	0.42
1:C:330:ILE:O	1:C:333:VAL:HG12	2.20	0.42
1:C:84:ILE:HD12	1:C:149:VAL:HG11	2.02	0.42
2:B:72:TYR:N	2:B:73:PRO:HD2	2.35	0.41
2:B:103:HIS:C	2:B:103:HIS:CD2	2.93	0.41
1:A:111:LYS:O	1:A:113:ARG:N	2.53	0.41
2:B:30:SER:N	2:B:31:GLU:OE1	2.53	0.41
1:A:62:GLU:C	1:A:64:LYS:H	2.22	0.41
1:C:80:PRO:O	1:C:84:ILE:HG12	2.20	0.41
2:D:7:VAL:HA	2:D:56:PHE:HB2	2.03	0.41
2:D:36:VAL:HG22	2:D:37:PHE:N	2.35	0.41
1:A:50:PRO:O	1:A:54:GLN:HG2	2.20	0.41
1:A:212:ARG:HA	1:A:215:LEU:CB	2.50	0.41
1:C:122:ARG:HA	1:C:229:VAL:HG11	2.02	0.41
2:D:11:ASP:OD2	2:D:89:SER:HA	2.20	0.41
1:A:111:LYS:CG	1:A:112:ARG:N	2.66	0.41
1:C:90:TYR:HE1	1:C:113:ARG:O	2.03	0.41
2:B:8:VAL:HG12	2:B:16:LYS:HD2	2.02	0.41
1:A:339:ASN:OD1	1:A:342:PHE:N	2.51	0.41
1:C:233:CYS:O	1:C:237:ILE:HG13	2.20	0.41
1:A:233:CYS:O	1:A:237:ILE:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:17:THR:OG1	2:D:35:THR:HG21	2.21	0.41
1:A:248:MET:SD	1:A:282:VAL:HG21	2.61	0.40
1:A:255:ASN:O	1:A:259:LEU:HD13	2.21	0.40
2:B:111:LEU:HD23	2:B:152:VAL:HB	2.02	0.40
1:A:69:CYS:O	1:A:73:ARG:HG3	2.21	0.40
2:D:79:LEU:HD22	2:D:113:VAL:HG21	2.03	0.40
1:A:80:PRO:O	1:A:84:ILE:HG12	2.22	0.40
1:C:310:MET:HG3	1:C:353:LEU:HB3	2.03	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	324/433 (75%)	304 (94%)	19 (6%)	1 (0%)	41 74
1	C	322/433 (74%)	314 (98%)	8 (2%)	0	100 100
2	B	176/181 (97%)	172 (98%)	4 (2%)	0	100 100
2	D	176/181 (97%)	173 (98%)	3 (2%)	0	100 100
All	All	998/1228 (81%)	963 (96%)	34 (3%)	1 (0%)	51 83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	251	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	249/377 (66%)	243 (98%)	6 (2%)	49	71
1	C	213/377 (56%)	202 (95%)	11 (5%)	23	54
2	B	138/159 (87%)	135 (98%)	3 (2%)	52	72
2	D	136/159 (86%)	135 (99%)	1 (1%)	84	91
All	All	736/1072 (69%)	715 (97%)	21 (3%)	42	67

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	114	VAL
1	A	152	GLU
1	A	211	SER
1	A	255	ASN
1	A	328	GLN
2	B	145	LEU
2	B	157	CYS
2	B	161	THR
1	C	34	GLU
1	C	37	GLU
1	C	39	PHE
1	C	54	GLN
1	C	113	ARG
1	C	115	GLN
1	C	152	GLU
1	C	249	ASN
1	C	256	GLU
1	C	336	SER
1	C	356	ASP
2	D	155	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	44	ASN
1	A	158	GLN
1	A	217	ASN

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Mol	Chain	Res	Type
2	B	103	HIS
2	B	116	GLN
1	C	115	GLN
1	C	228	HIS

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

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	GNP	D	201	4	29,34,34	2.04	11 (37%)	33,54,54	1.91	10 (30%)
3	GNP	B	201	4	29,34,34	1.85	11 (37%)	33,54,54	2.26	13 (39%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GNP	D	201	4	-	4/14/38/38	0/3/3/3
3	GNP	B	201	4	-	3/14/38/38	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	201	GNP	PG-O1G	4.78	1.53	1.46
3	D	201	GNP	PB-O1B	4.14	1.52	1.46
3	B	201	GNP	PG-O1G	3.88	1.52	1.46
3	B	201	GNP	PG-N3B	3.17	1.71	1.63
3	D	201	GNP	PG-N3B	3.15	1.71	1.63
3	D	201	GNP	C8-N7	-3.11	1.29	1.34
3	B	201	GNP	C8-N7	-3.06	1.29	1.34
3	D	201	GNP	PB-N3B	2.81	1.70	1.63
3	B	201	GNP	PB-N3B	2.79	1.70	1.63
3	B	201	GNP	PB-O1B	2.65	1.50	1.46
3	D	201	GNP	C3'-C4'	-2.63	1.46	1.53
3	B	201	GNP	C3'-C4'	-2.62	1.46	1.53
3	B	201	GNP	O3'-C3'	2.55	1.49	1.43
3	D	201	GNP	O3'-C3'	2.54	1.49	1.43
3	D	201	GNP	PB-O2B	-2.39	1.50	1.56
3	D	201	GNP	C5'-C4'	2.19	1.58	1.51
3	B	201	GNP	C5'-C4'	2.18	1.58	1.51
3	D	201	GNP	C6-N1	2.13	1.36	1.33
3	B	201	GNP	PG-O3G	-2.11	1.51	1.56
3	D	201	GNP	PG-O3G	-2.10	1.51	1.56
3	B	201	GNP	PA-O2A	-2.09	1.45	1.55
3	B	201	GNP	C6-N1	2.07	1.36	1.33

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	201	GNP	O1G-PG-N3B	-5.91	103.07	111.77
3	D	201	GNP	C5-C6-N1	-4.72	116.98	123.43
3	B	201	GNP	C5-C6-N1	-4.70	117.00	123.43
3	B	201	GNP	C2-N1-C6	3.86	122.07	115.93
3	D	201	GNP	C2-N1-C6	3.86	122.06	115.93
3	B	201	GNP	N3-C2-N1	-3.46	122.61	127.22
3	D	201	GNP	N3-C2-N1	-3.44	122.64	127.22
3	D	201	GNP	C2'-C3'-C4'	3.32	109.10	102.64
3	B	201	GNP	C2'-C3'-C4'	3.32	109.09	102.64
3	D	201	GNP	O2B-PB-O1B	2.88	115.95	109.92
3	B	201	GNP	O2B-PB-O1B	2.87	115.94	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	201	GNP	O1B-PB-N3B	-2.82	107.62	111.77
3	B	201	GNP	O2G-PG-O3G	2.70	114.83	107.64
3	B	201	GNP	O3A-PB-N3B	-2.68	99.15	106.59
3	D	201	GNP	O3A-PB-N3B	-2.67	99.17	106.59
3	B	201	GNP	O4'-C1'-C2'	2.29	110.27	106.93
3	D	201	GNP	O4'-C1'-C2'	2.28	110.26	106.93
3	B	201	GNP	O2'-C2'-C3'	2.14	118.73	111.82
3	B	201	GNP	C5'-C4'-C3'	-2.13	107.21	115.18
3	D	201	GNP	O2'-C2'-C3'	2.12	118.69	111.82
3	D	201	GNP	C5'-C4'-C3'	-2.12	107.23	115.18
3	B	201	GNP	O3'-C3'-C2'	-2.05	105.20	111.82
3	D	201	GNP	O3'-C3'-C2'	-2.03	105.25	111.82

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	201	GNP	PG-N3B-PB-O1B
3	B	201	GNP	PA-O3A-PB-O1B
3	B	201	GNP	PA-O3A-PB-O2B
3	D	201	GNP	PB-N3B-PG-O1G
3	D	201	GNP	PA-O3A-PB-O1B
3	D	201	GNP	PA-O3A-PB-O2B
3	D	201	GNP	PG-N3B-PB-O1B

There are no ring outliers.

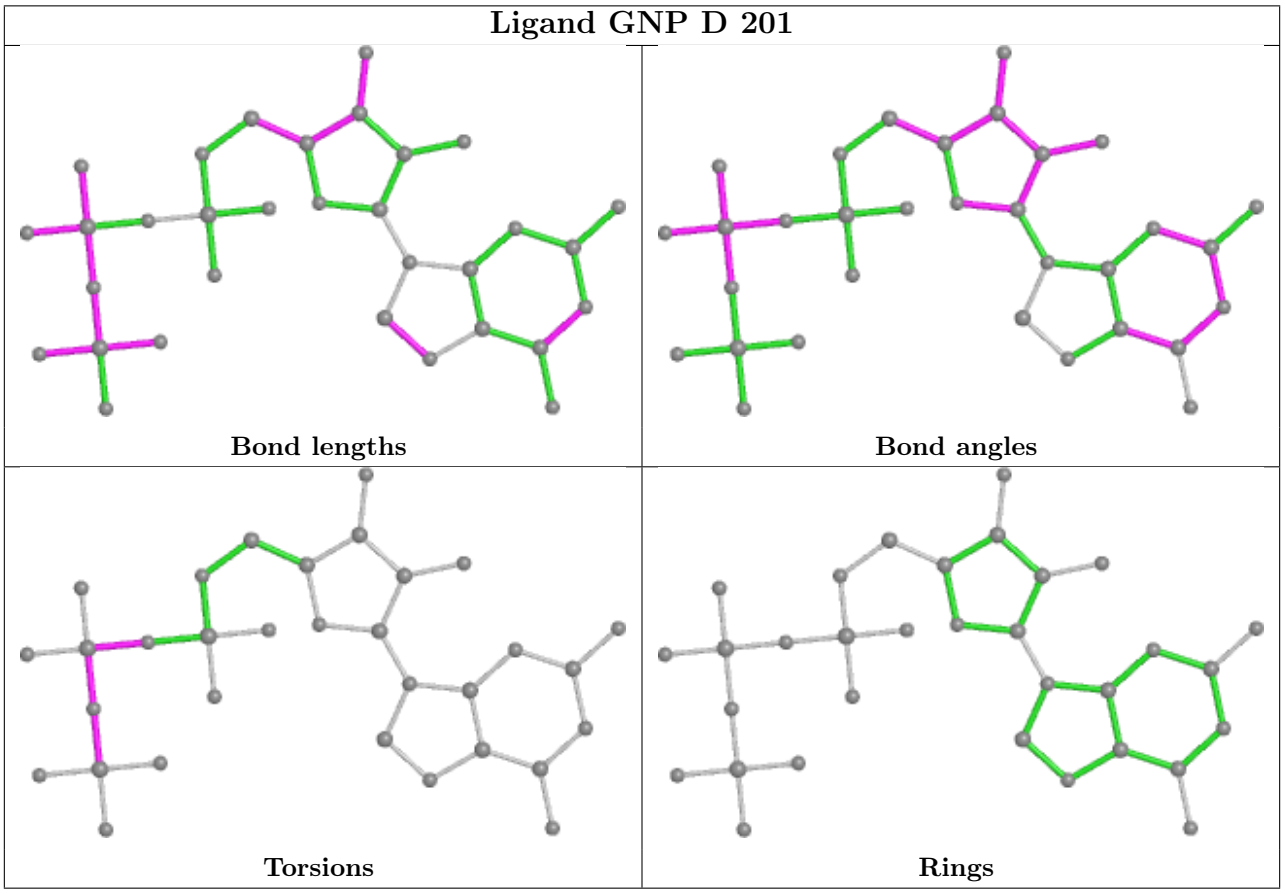
2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	201	GNP	4	0
3	B	201	GNP	6	0

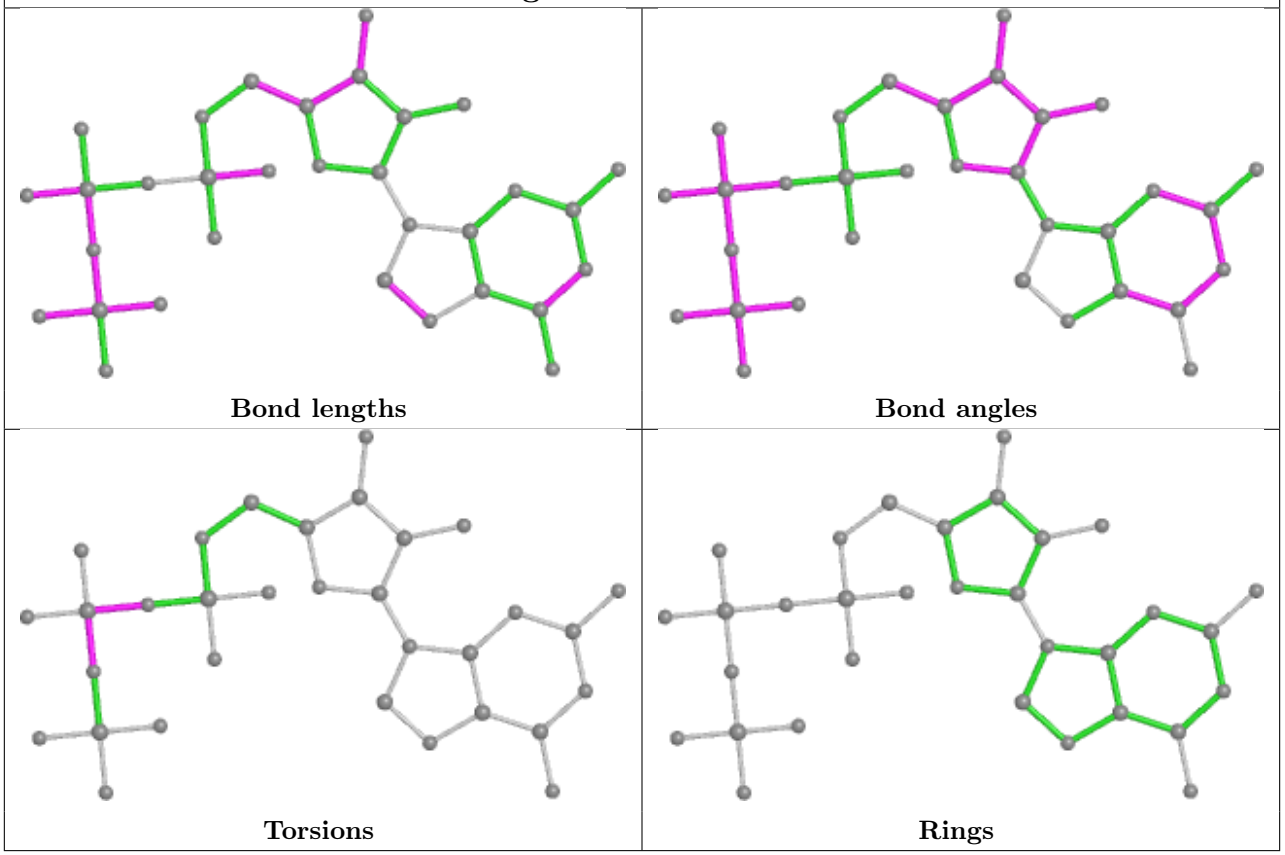
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GNP D 201



Ligand GNP B 201



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	330/433 (76%)	-0.21	6 (1%) 68 61	66, 100, 186, 223	0
1	C	328/433 (75%)	-0.15	13 (3%) 38 32	69, 97, 185, 222	0
2	B	178/181 (98%)	-0.31	0 100 100	57, 88, 111, 142	0
2	D	178/181 (98%)	-0.34	0 100 100	70, 95, 125, 147	0
All	All	1014/1228 (82%)	-0.23	19 (1%) 66 59	57, 96, 170, 223	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	413	GLU	4.5
1	C	412	THR	3.8
1	C	414	ARG	3.4
1	A	412	THR	3.2
1	C	411	LEU	3.0
1	C	162	THR	2.8
1	C	418	ALA	2.8
1	A	417	ASP	2.6
1	C	420	ASN	2.5
1	C	416	ARG	2.4
1	C	164	ASP	2.4
1	C	417	ASP	2.3
1	A	420	ASN	2.3
1	C	161	VAL	2.2
1	A	422	SER	2.2
1	C	419	GLU	2.1
1	C	409	ALA	2.1
1	A	415	LEU	2.1
1	A	411	LEU	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

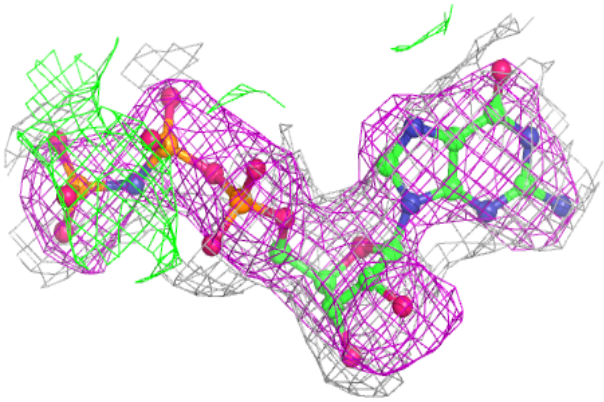
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

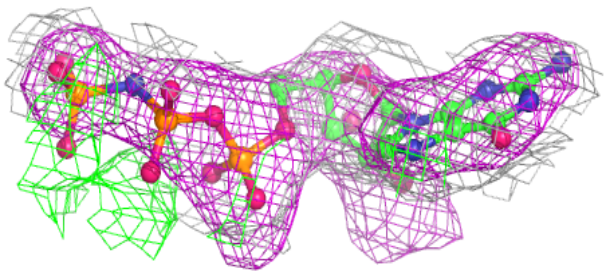
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GNP	D	201	32/32	0.88	0.25	7,10,13,15	0
3	GNP	B	201	32/32	0.91	0.22	7,10,13,15	0
4	MG	D	202	1/1	0.91	0.23	92,92,92,92	0
4	MG	B	202	1/1	0.92	0.20	73,73,73,73	0

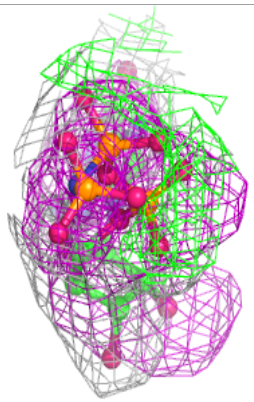
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GNP D 201:

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

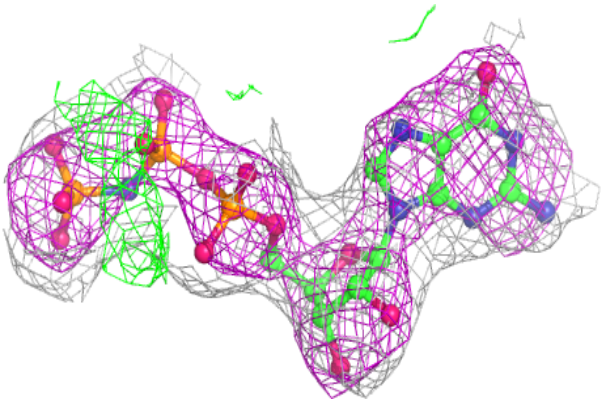


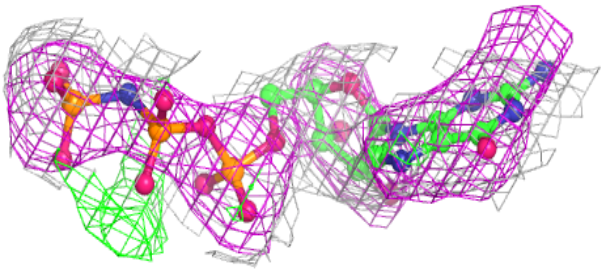


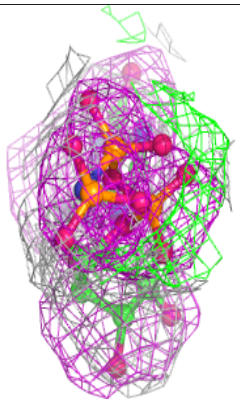


Electron density around GNP B 201:

$2mF_o$-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.