



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:27 AM UTC

PDB ID : 1CJB / pdb_00001cjb
Title : MALARIAL PURINE PHOSPHORIBOSYLTRANSFERASE
Authors : Shi, W.; Li, C.M.; Tyler, P.C.; Furneaux, R.H.; Cahill, S.M.; Girvin, M.E.;
Grubmeyer, C.; Schramm, V.L.; Almo, S.C.
Deposited on : 1999-04-08
Resolution : 2.00 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

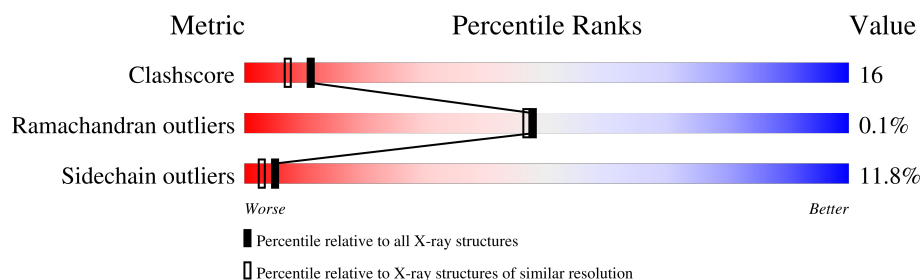
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	231	
1	B	231	
1	C	231	
1	D	231	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7876 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.

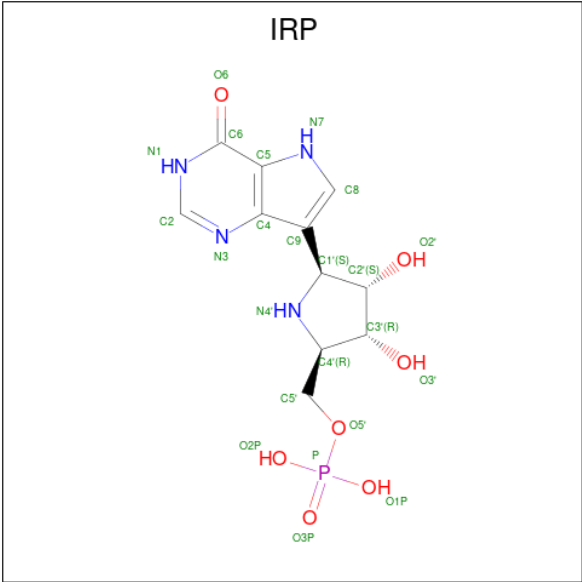
- Molecule 1 is a protein called PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	1
			1828	1186	301	333	8			
1	B	228	Total	C	N	O	S	0	0	1
			1828	1186	301	333	8			
1	C	230	Total	C	N	O	S	0	0	0
			1849	1199	303	339	8			
1	D	228	Total	C	N	O	S	0	0	1
			1828	1186	301	333	8			

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

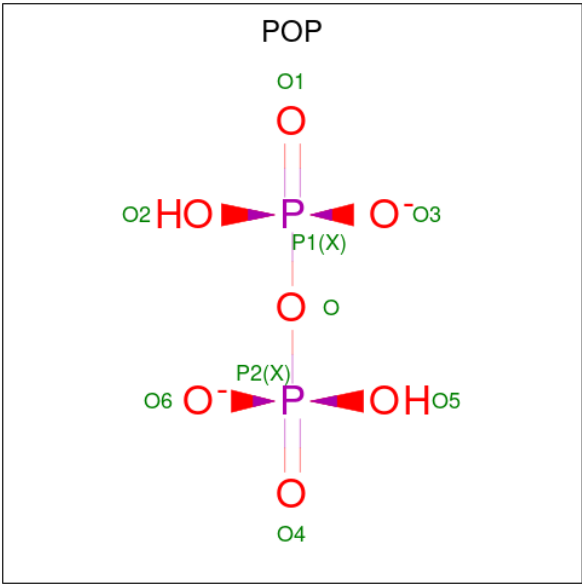
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		
2	C	2	Total	Mg	0	0
			2	2		
2	D	2	Total	Mg	0	0
			2	2		

- Molecule 3 is (1S)-1(9-DEAZAHYPOXANTHIN-9YL)1,4-DIDEOXY-1,4-IMINO-D-RIBITOL-5-PHOSPHATE (CCD ID: IRP) (formula: C₁₁H₁₅N₄O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	11	4	7	1		
3	B	1	Total	C	N	O	P	0	0
			23	11	4	7	1		
3	C	1	Total	C	N	O	P	0	0
			23	11	4	7	1		
3	D	1	Total	C	N	O	P	0	0
			23	11	4	7	1		

- Molecule 4 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 9 7 2	0	0
4	B	1	Total O P 9 7 2	0	0
4	C	1	Total O P 9 7 2	0	0
4	D	1	Total O P 9 7 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	118	Total O 118 118	0	0
5	B	128	Total O 128 128	0	0
5	C	92	Total O 92 92	0	0
5	D	69	Total O 69 69	0	0

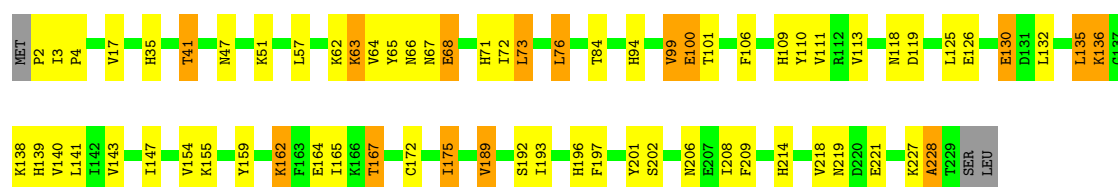
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

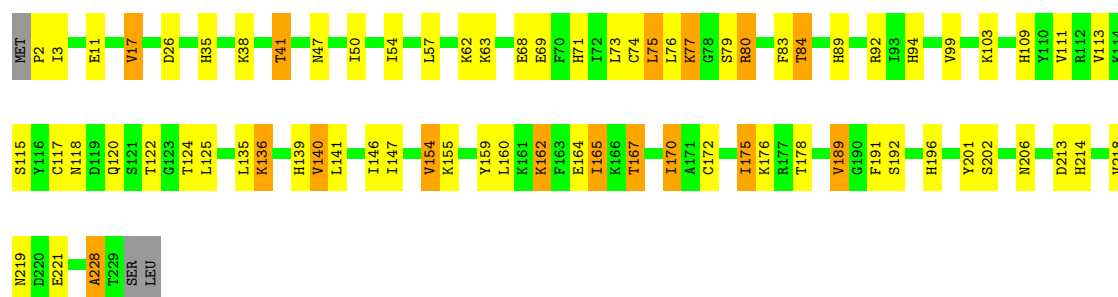
- Molecule 1: PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE)

Chain A: 



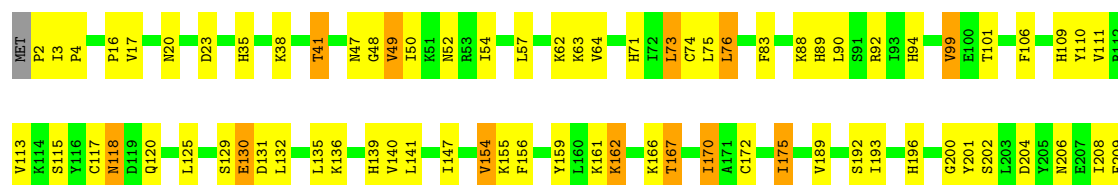
- Molecule 1: PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE)

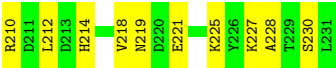
Chain B: 



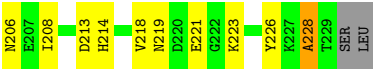
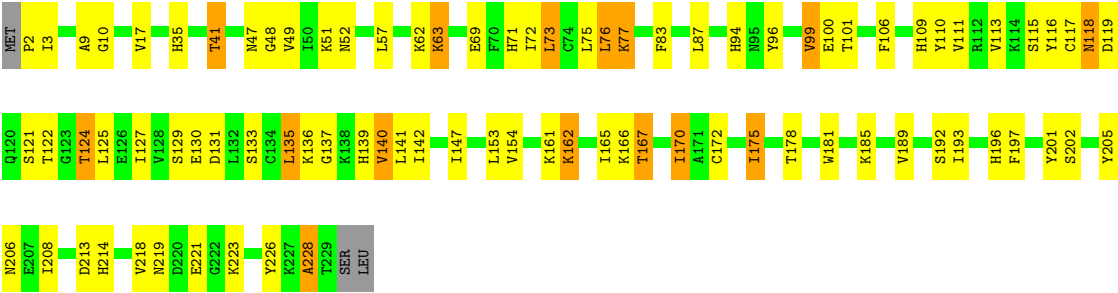
- Molecule 1: PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE)

Chain C: 





● Molecule 1: PROTEIN (HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	105.49Å 110.39Å 173.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	98.0 (20.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.196 , 0.239	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7876	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.43	1/1872 (0.1%)	0.92	5/2529 (0.2%)
1	B	0.45	1/1872 (0.1%)	0.93	6/2529 (0.2%)
1	C	0.39	0/1893	0.90	6/2556 (0.2%)
1	D	0.42	1/1872 (0.1%)	0.90	7/2529 (0.3%)
All	All	0.42	3/7509 (0.0%)	0.91	24/10143 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	228	ALA	C-N	-5.52	1.25	1.33
1	A	228	ALA	C-N	-5.49	1.25	1.33
1	D	228	ALA	C-N	-5.41	1.25	1.33

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	193	ILE	N-CA-C	7.71	116.40	107.84
1	B	17	VAL	N-CA-C	-6.65	101.00	109.58
1	D	193	ILE	N-CA-C	6.61	115.18	107.84
1	A	130	GLU	N-CA-C	-6.12	102.45	110.53
1	C	193	ILE	N-CA-C	6.08	114.59	107.84
1	D	2	PRO	N-CA-CB	6.05	109.66	103.00
1	C	106	PHE	N-CA-C	6.03	118.13	109.14
1	D	17	VAL	N-CA-C	-5.99	101.85	109.58
1	A	2	PRO	N-CA-CB	5.92	109.51	103.00
1	B	146	ILE	N-CA-C	5.81	115.49	108.06
1	C	2	PRO	N-CA-CB	5.79	109.37	103.00
1	B	2	PRO	N-CA-CB	5.78	109.36	103.00
1	B	170	ILE	N-CA-C	5.73	116.25	107.77
1	A	106	PHE	N-CA-C	5.71	117.75	109.07

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	17	VAL	N-CA-C	-5.65	102.23	109.30
1	A	17	VAL	N-CA-C	-5.55	102.36	109.30
1	C	118	ASN	CB-CA-C	-5.38	110.39	116.63
1	D	213	ASP	N-CA-C	5.36	117.20	111.36
1	D	106	PHE	N-CA-C	5.35	117.11	109.14
1	D	170	ILE	N-CA-C	5.31	115.55	108.11
1	B	11	GLU	N-CA-C	5.28	117.72	111.33
1	C	170	ILE	N-CA-C	5.28	115.50	108.11
1	B	213	ASP	N-CA-C	5.28	117.04	111.28
1	D	118	ASN	CB-CA-C	-5.20	110.60	116.63

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1828	0	1822	61	0
1	B	1828	0	1822	57	0
1	C	1849	0	1845	66	0
1	D	1828	0	1822	73	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	23	0	12	0	0
3	B	23	0	11	0	0
3	C	23	0	12	0	0
3	D	23	0	12	0	0
4	A	9	0	0	0	0
4	B	9	0	0	0	0
4	C	9	0	0	0	0
4	D	9	0	0	0	0
5	A	118	0	0	6	0
5	B	128	0	0	7	0
5	C	92	0	0	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	69	0	0	5	0
All	All	7876	0	7358	244	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 16.

All (244) 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:118:ASN:HD21	1:C:228:ALA:H	1.10	0.99
1:C:47:ASN:H	1:C:214:HIS:HD2	1.07	0.96
1:D:47:ASN:H	1:D:214:HIS:HD2	1.10	0.94
1:C:48:GLY:H	1:D:52:ASN:HD21	1.13	0.94
1:B:118:ASN:HD21	1:B:228:ALA:H	1.09	0.94
1:C:52:ASN:HD21	1:D:48:GLY:H	1.15	0.92
1:A:47:ASN:H	1:A:214:HIS:HD2	1.06	0.92
1:C:139:HIS:HD2	1:C:167:THR:HB	1.33	0.90
1:D:118:ASN:HD21	1:D:228:ALA:H	1.15	0.90
1:B:113:VAL:HG13	1:B:125:LEU:HD11	1.51	0.89
1:D:118:ASN:HD22	1:D:206:ASN:HD21	1.20	0.88
1:A:41:THR:HG22	1:A:219:ASN:HB3	1.56	0.88
1:B:47:ASN:H	1:B:214:HIS:HD2	1.23	0.87
1:D:111:VAL:HG13	1:D:129:SER:HB3	1.56	0.87
1:C:41:THR:HG22	1:C:219:ASN:HB3	1.59	0.84
1:D:47:ASN:H	1:D:214:HIS:CD2	1.95	0.84
1:B:41:THR:HG22	1:B:219:ASN:HB3	1.60	0.83
1:A:118:ASN:HD22	1:A:206:ASN:HD21	1.26	0.82
1:B:113:VAL:CG1	1:B:125:LEU:HD11	2.10	0.82
1:B:139:HIS:HD2	1:B:167:THR:HB	1.44	0.81
1:C:118:ASN:HD22	1:C:206:ASN:HD21	1.27	0.81
1:A:118:ASN:HD21	1:A:228:ALA:H	1.24	0.81
1:C:47:ASN:H	1:C:214:HIS:CD2	1.98	0.79
1:A:139:HIS:HD2	1:A:167:THR:HB	1.48	0.78
1:C:113:VAL:CG1	1:C:125:LEU:HD11	2.15	0.77
1:C:52:ASN:ND2	1:D:48:GLY:H	1.81	0.76
1:C:48:GLY:H	1:D:52:ASN:ND2	1.84	0.76
1:A:118:ASN:ND2	1:A:206:ASN:HD21	1.83	0.76
1:B:38:LYS:HE3	5:B:804:HOH:O	1.87	0.74
1:D:118:ASN:ND2	1:D:206:ASN:HD21	1.85	0.74
1:A:47:ASN:H	1:A:214:HIS:CD2	1.99	0.73
1:C:62:LYS:NZ	1:C:94:HIS:HD2	1.86	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:VAL:HG22	1:D:49:VAL:HG23	1.70	0.72
1:A:71:HIS:HD2	1:A:109:HIS:HE1	1.38	0.71
1:C:167:THR:HG22	5:C:519:HOH:O	1.91	0.70
1:A:196:HIS:HE1	5:A:775:HOH:O	1.73	0.70
1:D:139:HIS:HA	1:D:167:THR:HG22	1.74	0.70
1:D:111:VAL:HG22	1:D:129:SER:HB2	1.74	0.69
1:C:71:HIS:CD2	1:C:109:HIS:HE1	2.09	0.69
1:D:71:HIS:HD2	1:D:109:HIS:HE1	1.41	0.69
1:B:118:ASN:ND2	1:B:206:ASN:HD21	1.91	0.68
1:C:118:ASN:ND2	1:C:228:ALA:H	1.88	0.68
1:B:118:ASN:HD22	1:B:206:ASN:HD21	1.42	0.67
1:D:41:THR:HG22	1:D:219:ASN:HB3	1.77	0.67
1:B:71:HIS:HD2	1:B:109:HIS:HE1	1.41	0.66
1:D:71:HIS:CD2	1:D:109:HIS:HE1	2.12	0.66
1:C:71:HIS:HD2	1:C:109:HIS:HE1	1.41	0.66
1:A:71:HIS:CD2	1:A:109:HIS:HE1	2.14	0.66
1:C:113:VAL:HG13	1:C:125:LEU:HD11	1.78	0.66
1:C:201:TYR:O	1:C:202:SER:HB2	1.95	0.65
1:C:52:ASN:HD21	1:D:48:GLY:N	1.92	0.65
1:C:38:LYS:HE3	5:C:587:HOH:O	1.96	0.65
1:C:49:VAL:HG22	1:D:49:VAL:CG2	2.27	0.65
1:C:147:ILE:HB	1:C:175:ILE:HG12	1.78	0.65
1:C:118:ASN:ND2	1:C:206:ASN:HD21	1.94	0.65
1:A:41:THR:HG21	5:A:901:HOH:O	1.97	0.64
1:A:3:ILE:HG21	1:A:167:THR:HG21	1.80	0.64
1:B:139:HIS:CD2	1:B:167:THR:HB	2.30	0.63
1:B:201:TYR:O	1:B:202:SER:HB2	1.98	0.62
1:B:62:LYS:NZ	1:B:94:HIS:HD2	1.97	0.62
1:A:62:LYS:NZ	1:A:94:HIS:HD2	1.96	0.62
1:D:175:ILE:HG22	1:D:192:SER:HA	1.82	0.61
1:A:136:LYS:HG3	1:A:164:GLU:HB2	1.81	0.61
1:B:47:ASN:H	1:B:214:HIS:CD2	2.11	0.61
1:B:71:HIS:CD2	1:B:109:HIS:HE1	2.18	0.60
1:D:62:LYS:NZ	1:D:94:HIS:HD2	1.99	0.60
1:D:201:TYR:O	1:D:202:SER:HB2	2.01	0.60
1:A:147:ILE:HG13	1:A:172:CYS:SG	2.42	0.60
1:B:75:LEU:O	1:B:79:SER:HB2	2.01	0.59
1:A:41:THR:HG22	1:A:219:ASN:CB	2.32	0.59
1:C:73:LEU:HD21	1:C:111:VAL:HG23	1.85	0.59
1:B:160:LEU:HD22	1:B:165:ILE:CD1	2.33	0.58
1:B:139:HIS:HD2	1:B:167:THR:CB	2.15	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:LYS:HZ3	1:C:94:HIS:HD2	1.49	0.58
1:C:48:GLY:N	1:D:52:ASN:HD21	1.94	0.58
1:C:74:CYS:HB2	1:C:83:PHE:CD1	2.38	0.58
1:D:181:TRP:HH2	1:D:185:LYS:HE3	1.68	0.58
1:B:118:ASN:HD21	1:B:228:ALA:N	1.92	0.58
1:B:167:THR:CG2	5:B:506:HOH:O	2.52	0.57
1:A:167:THR:CG2	5:A:525:HOH:O	2.51	0.57
1:A:35:HIS:H	1:A:35:HIS:CD2	2.22	0.57
1:D:47:ASN:N	1:D:214:HIS:HD2	1.91	0.57
1:B:35:HIS:CD2	1:B:35:HIS:H	2.23	0.56
1:B:175:ILE:HG22	1:B:192:SER:HA	1.87	0.56
1:C:16:PRO:HB3	1:C:189:VAL:HG13	1.87	0.56
1:B:69:GLU:OE2	1:B:71:HIS:HE1	1.87	0.56
1:A:147:ILE:HB	1:A:175:ILE:HG12	1.87	0.56
1:D:118:ASN:HD21	1:D:228:ALA:N	1.96	0.55
1:A:113:VAL:CG1	1:A:125:LEU:HD11	2.37	0.55
1:A:73:LEU:HD21	1:A:111:VAL:HG23	1.89	0.55
1:B:136:LYS:HE3	1:B:164:GLU:HB2	1.89	0.55
1:C:147:ILE:HG13	1:C:172:CYS:SG	2.47	0.55
1:D:116:TYR:CE1	1:D:121:SER:HB2	2.41	0.55
1:D:137:GLY:C	1:D:166:LYS:HB2	2.32	0.54
1:A:100:GLU:OE2	1:B:38:LYS:HE2	2.07	0.54
1:B:122:THR:OG1	1:B:124:THR:HG22	2.08	0.54
1:B:176:LYS:HE2	1:B:196:HIS:O	2.08	0.54
1:A:63:LYS:HE3	5:A:710:HOH:O	2.07	0.54
1:D:147:ILE:HG12	1:D:153:LEU:HD12	1.89	0.54
1:D:139:HIS:HD2	1:D:167:THR:CG2	2.21	0.53
1:A:3:ILE:CG2	1:A:167:THR:HG21	2.38	0.53
1:A:139:HIS:HD2	1:A:167:THR:CB	2.20	0.53
1:B:147:ILE:HB	1:B:175:ILE:HG12	1.89	0.53
1:C:196:HIS:HE1	5:C:630:HOH:O	1.91	0.53
1:C:139:HIS:CD2	1:C:167:THR:HB	2.26	0.53
1:B:89:HIS:HD2	1:B:92:ARG:HH21	1.57	0.52
1:D:139:HIS:HD2	1:D:167:THR:HB	1.75	0.52
1:C:88:LYS:HE3	1:C:92:ARG:HH12	1.74	0.52
1:D:47:ASN:O	1:D:51:LYS:HG2	2.10	0.52
1:C:172:CYS:O	1:C:189:VAL:HA	2.10	0.51
1:A:84:THR:HG21	1:B:84:THR:HG23	1.91	0.51
1:B:3:ILE:HG21	1:B:167:THR:HG21	1.91	0.51
1:A:84:THR:HG21	1:B:84:THR:CG2	2.40	0.51
1:D:35:HIS:CD2	1:D:35:HIS:H	2.27	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:HIS:CD2	1:A:167:THR:HB	2.37	0.51
1:A:201:TYR:O	1:A:202:SER:HB2	2.11	0.51
1:C:41:THR:HG22	1:C:219:ASN:CB	2.37	0.51
1:D:113:VAL:CG1	1:D:125:LEU:HD11	2.41	0.51
1:B:68:GLU:HG2	5:B:733:HOH:O	2.10	0.50
1:D:71:HIS:HD2	1:D:109:HIS:CE1	2.27	0.50
1:D:99:VAL:HG13	1:D:100:GLU:N	2.26	0.50
1:D:73:LEU:CD2	1:D:111:VAL:HG23	2.42	0.50
1:B:73:LEU:HD21	1:B:111:VAL:CG2	2.42	0.49
1:B:74:CYS:HB2	1:B:83:PHE:CE1	2.47	0.49
1:B:154:VAL:HG12	1:B:155:LYS:N	2.26	0.49
1:B:62:LYS:HZ3	1:B:94:HIS:HD2	1.58	0.49
1:D:115:SER:HB3	1:D:125:LEU:HD12	1.94	0.49
1:A:62:LYS:HZ2	1:A:94:HIS:HD2	1.59	0.49
1:C:50:ILE:O	1:C:54:ILE:HG13	2.13	0.49
1:A:72:ILE:HG23	1:A:143:VAL:CG2	2.44	0.48
1:C:74:CYS:HB2	1:C:83:PHE:CE1	2.49	0.48
1:D:172:CYS:O	1:D:189:VAL:HA	2.14	0.48
1:B:26:ASP:OD2	5:B:903:HOH:O	2.20	0.48
1:D:139:HIS:CD2	1:D:167:THR:CG2	2.97	0.48
1:D:196:HIS:HE1	5:D:884:HOH:O	1.96	0.48
1:A:154:VAL:HG13	1:A:155:LYS:N	2.29	0.47
1:A:35:HIS:CE1	5:B:674:HOH:O	2.67	0.47
1:C:175:ILE:HG22	1:C:192:SER:HA	1.96	0.47
1:A:99:VAL:HG13	1:A:100:GLU:N	2.29	0.47
1:C:99:VAL:HG13	1:C:101:THR:H	1.79	0.47
1:D:140:VAL:HG13	1:D:165:ILE:HG21	1.96	0.47
1:A:72:ILE:HG23	1:A:143:VAL:HG23	1.96	0.47
1:A:66:ASN:HB3	1:A:67:ASN:H	1.54	0.47
1:C:89:HIS:HD2	1:C:92:ARG:NH2	2.13	0.47
1:D:139:HIS:CA	1:D:167:THR:HG22	2.43	0.47
1:D:122:THR:OG1	1:D:124:THR:HG22	2.15	0.47
1:C:208:ILE:O	1:C:209:PHE:HB2	2.15	0.47
1:C:62:LYS:NZ	1:C:94:HIS:CD2	2.76	0.47
1:A:110:TYR:OH	1:B:80:ARG:HG3	2.15	0.46
1:C:3:ILE:CG2	1:C:167:THR:HG21	2.45	0.46
1:D:167:THR:HG23	5:D:571:HOH:O	2.15	0.46
1:C:35:HIS:H	1:C:35:HIS:CD2	2.31	0.46
1:C:49:VAL:CG2	1:D:49:VAL:CG2	2.93	0.46
1:A:113:VAL:HG12	1:A:125:LEU:HD11	1.97	0.46
1:A:135:LEU:HB3	1:A:165:ILE:HG12	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:208:ILE:HG13	1:D:226:TYR:CD1	2.50	0.46
1:A:73:LEU:CD2	1:A:111:VAL:HG23	2.44	0.46
1:A:76:LEU:HD22	1:A:110:TYR:HB3	1.98	0.46
1:A:172:CYS:O	1:A:189:VAL:HA	2.16	0.46
1:A:175:ILE:HG22	1:A:192:SER:HA	1.97	0.46
1:B:89:HIS:CD2	1:B:92:ARG:HH21	2.33	0.46
1:D:113:VAL:HG22	1:D:127:ILE:HG12	1.97	0.46
1:A:63:LYS:HE2	5:A:510:HOH:O	2.16	0.46
1:C:159:TYR:O	1:C:162:LYS:HG3	2.15	0.46
1:D:62:LYS:HZ3	1:D:94:HIS:HD2	1.63	0.46
1:B:159:TYR:O	1:B:162:LYS:HG3	2.15	0.46
1:D:76:LEU:HA	1:D:77:LYS:HA	1.59	0.45
1:A:136:LYS:HE3	1:A:164:GLU:HG3	1.98	0.45
1:A:154:VAL:CG1	1:A:155:LYS:N	2.79	0.45
1:B:89:HIS:CD2	1:B:92:ARG:NH2	2.84	0.45
1:A:119:ASP:HA	1:A:197:PHE:CE1	2.52	0.45
1:D:135:LEU:HB3	1:D:165:ILE:HG12	1.99	0.45
1:C:115:SER:HB3	1:C:125:LEU:HD12	1.99	0.45
1:D:140:VAL:HG13	1:D:165:ILE:CG2	2.47	0.45
1:D:63:LYS:HE2	5:D:589:HOH:O	2.16	0.44
1:A:118:ASN:HD22	1:A:206:ASN:ND2	2.06	0.44
1:A:136:LYS:HE3	1:A:164:GLU:HB2	1.99	0.44
5:A:619:HOH:O	1:B:77:LYS:HB2	2.17	0.44
1:B:117:CYS:O	1:B:118:ASN:HB2	2.18	0.44
1:B:140:VAL:HG13	1:B:165:ILE:CG2	2.47	0.44
1:C:117:CYS:O	1:C:118:ASN:HB2	2.18	0.44
1:D:117:CYS:O	1:D:118:ASN:HB2	2.18	0.44
1:B:69:GLU:OE2	1:B:71:HIS:CE1	2.69	0.44
1:C:3:ILE:HG22	1:C:167:THR:HG21	1.99	0.44
1:D:9:ALA:O	1:D:10:GLY:C	2.59	0.44
1:A:4:PRO:HD3	1:A:64:VAL:HG11	2.00	0.44
1:B:50:ILE:O	1:B:54:ILE:HG13	2.18	0.44
1:D:162:LYS:H	1:D:162:LYS:HG2	1.39	0.44
1:A:47:ASN:HD21	1:A:51:LYS:NZ	2.16	0.44
1:C:154:VAL:HG12	1:C:155:LYS:N	2.31	0.44
1:D:76:LEU:HD22	1:D:110:TYR:HB3	1.99	0.43
1:D:3:ILE:HG21	1:D:167:THR:HG21	1.99	0.43
1:D:167:THR:CG2	5:D:571:HOH:O	2.65	0.43
1:D:72:ILE:CG2	1:D:83:PHE:HE1	2.32	0.43
1:C:130:GLU:O	1:C:132:LEU:HG	2.19	0.43
1:A:159:TYR:O	1:A:162:LYS:HG3	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:GLY:HA2	1:C:212:LEU:HB3	2.01	0.43
1:C:113:VAL:HG13	1:C:125:LEU:CD1	2.47	0.43
1:C:62:LYS:HZ1	1:C:94:HIS:HD2	1.64	0.42
1:C:167:THR:CG2	5:C:519:HOH:O	2.59	0.42
1:B:76:LEU:HA	1:B:77:LYS:HA	1.70	0.42
1:B:167:THR:HG22	5:B:506:HOH:O	2.18	0.42
1:A:51:LYS:HZ2	1:A:51:LYS:HG3	1.63	0.42
1:B:136:LYS:HE2	1:B:164:GLU:OE2	2.19	0.42
1:D:51:LYS:HZ2	1:D:51:LYS:HG3	1.50	0.42
1:A:109:HIS:HD2	1:A:130:GLU:OE2	2.02	0.42
1:C:130:GLU:O	1:C:132:LEU:N	2.52	0.42
1:D:111:VAL:HG22	1:D:129:SER:CB	2.46	0.42
1:D:139:HIS:HD2	1:D:167:THR:CB	2.32	0.42
1:B:196:HIS:HE1	5:B:683:HOH:O	2.01	0.42
1:C:162:LYS:H	1:C:162:LYS:HG2	1.56	0.42
1:D:175:ILE:O	1:D:175:ILE:CG2	2.68	0.42
1:B:17:VAL:HB	1:B:191:PHE:CD2	2.54	0.42
1:C:4:PRO:HD3	1:C:64:VAL:HG11	2.02	0.41
1:C:62:LYS:HZ1	1:C:94:HIS:CD2	2.38	0.41
1:A:99:VAL:HG13	1:A:101:THR:H	1.84	0.41
1:B:3:ILE:CG2	1:B:167:THR:HG21	2.50	0.41
1:B:3:ILE:HD11	1:B:68:GLU:HG2	2.02	0.41
1:D:119:ASP:HA	1:D:197:PHE:CE1	2.55	0.41
1:A:208:ILE:O	1:A:209:PHE:HB2	2.21	0.41
1:C:76:LEU:HD22	1:C:110:TYR:HB3	2.03	0.41
1:D:41:THR:HG22	1:D:219:ASN:CB	2.47	0.41
1:D:73:LEU:HD21	1:D:111:VAL:HG23	2.02	0.41
1:A:71:HIS:CE1	1:A:138:LYS:HD2	2.55	0.41
1:D:47:ASN:ND2	5:D:888:HOH:O	2.44	0.41
1:D:147:ILE:CG1	1:D:153:LEU:HD12	2.50	0.41
1:A:99:VAL:CG1	1:A:101:THR:H	2.34	0.41
1:B:115:SER:HB3	1:B:125:LEU:HD12	2.03	0.41
1:C:89:HIS:CD2	1:C:92:ARG:NH2	2.89	0.41
1:C:111:VAL:HG11	1:C:156:PHE:CE1	2.55	0.41
1:C:204:ASP:HB3	1:C:210:ARG:HG2	2.03	0.41
1:C:20:ASN:HB2	1:C:23:ASP:CG	2.46	0.41
1:B:74:CYS:HB2	1:B:83:PHE:CD1	2.56	0.40
1:A:65:TYR:O	1:A:68:GLU:HB2	2.21	0.40
1:D:99:VAL:CG1	1:D:100:GLU:N	2.84	0.40
1:A:139:HIS:HD2	1:A:167:THR:CG2	2.34	0.40
1:D:131:ASP:OD1	1:D:133:SER:HB3	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:ILE:HD12	1:D:170:ILE:HD13	2.02	0.40
1:D:205:TYR:CE2	1:D:223:LYS:HA	2.56	0.40
1:A:132:LEU:HD12	1:A:159:TYR:HE2	1.85	0.40
1:C:111:VAL:HG12	1:C:113:VAL:HG23	2.03	0.40
1:D:99:VAL:CG1	1:D:101:THR:H	2.35	0.40
1:B:172:CYS:O	1:B:189:VAL:HA	2.22	0.40
1:C:90:LEU:HD23	1:C:90:LEU:HA	1.96	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	226/231 (98%)	217 (96%)	9 (4%)	0	100	100
1	B	226/231 (98%)	218 (96%)	8 (4%)	0	100	100
1	C	228/231 (99%)	219 (96%)	8 (4%)	1 (0%)	30	27
1	D	226/231 (98%)	216 (96%)	10 (4%)	0	100	100
All	All	906/924 (98%)	870 (96%)	35 (4%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	131	ASP

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	202/207 (98%)	182 (90%)	20 (10%)	7	4
1	B	202/207 (98%)	178 (88%)	24 (12%)	5	3
1	C	205/207 (99%)	178 (87%)	27 (13%)	4	2
1	D	202/207 (98%)	177 (88%)	25 (12%)	4	2
All	All	811/828 (98%)	715 (88%)	96 (12%)	5	3

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	57	LEU
1	A	63	LYS
1	A	68	GLU
1	A	73	LEU
1	A	76	LEU
1	A	99	VAL
1	A	100	GLU
1	A	126	GLU
1	A	135	LEU
1	A	136	LYS
1	A	140	VAL
1	A	141	LEU
1	A	162	LYS
1	A	167	THR
1	A	175	ILE
1	A	189	VAL
1	A	218	VAL
1	A	221	GLU
1	A	227	LYS
1	B	41	THR
1	B	57	LEU
1	B	63	LYS
1	B	75	LEU
1	B	77	LYS
1	B	80	ARG
1	B	84	THR
1	B	99	VAL
1	B	103	LYS
1	B	120	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	135	LEU
1	B	136	LYS
1	B	140	VAL
1	B	141	LEU
1	B	154	VAL
1	B	162	LYS
1	B	165	ILE
1	B	167	THR
1	B	170	ILE
1	B	175	ILE
1	B	178	THR
1	B	189	VAL
1	B	218	VAL
1	B	221	GLU
1	C	41	THR
1	C	49	VAL
1	C	57	LEU
1	C	63	LYS
1	C	73	LEU
1	C	75	LEU
1	C	76	LEU
1	C	99	VAL
1	C	120	GLN
1	C	129	SER
1	C	130	GLU
1	C	135	LEU
1	C	136	LYS
1	C	140	VAL
1	C	141	LEU
1	C	154	VAL
1	C	161	LYS
1	C	162	LYS
1	C	166	LYS
1	C	167	THR
1	C	170	ILE
1	C	175	ILE
1	C	218	VAL
1	C	221	GLU
1	C	225	LYS
1	C	227	LYS
1	C	230	SER
1	D	41	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	57	LEU
1	D	63	LYS
1	D	69	GLU
1	D	73	LEU
1	D	75	LEU
1	D	76	LEU
1	D	77	LYS
1	D	87	LEU
1	D	96	TYR
1	D	99	VAL
1	D	124	THR
1	D	130	GLU
1	D	135	LEU
1	D	136	LYS
1	D	140	VAL
1	D	141	LEU
1	D	154	VAL
1	D	161	LYS
1	D	162	LYS
1	D	167	THR
1	D	175	ILE
1	D	178	THR
1	D	218	VAL
1	D	221	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	20	ASN
1	A	35	HIS
1	A	47	ASN
1	A	71	HIS
1	A	89	HIS
1	A	94	HIS
1	A	109	HIS
1	A	118	ASN
1	A	139	HIS
1	A	196	HIS
1	A	214	HIS
1	B	6	ASN
1	B	20	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	35	HIS
1	B	71	HIS
1	B	89	HIS
1	B	94	HIS
1	B	109	HIS
1	B	118	ASN
1	B	139	HIS
1	B	196	HIS
1	B	214	HIS
1	C	6	ASN
1	C	20	ASN
1	C	35	HIS
1	C	47	ASN
1	C	52	ASN
1	C	71	HIS
1	C	89	HIS
1	C	94	HIS
1	C	109	HIS
1	C	118	ASN
1	C	139	HIS
1	C	196	HIS
1	C	214	HIS
1	D	6	ASN
1	D	20	ASN
1	D	35	HIS
1	D	47	ASN
1	D	52	ASN
1	D	71	HIS
1	D	89	HIS
1	D	94	HIS
1	D	109	HIS
1	D	118	ASN
1	D	139	HIS
1	D	214	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	POP	B	400	2	6,8,8	1.47	1 (16%)	12,13,13	0.99	2 (16%)
4	POP	D	400	2	6,8,8	1.42	0	12,13,13	0.91	1 (8%)
3	IRP	D	300	2	25,25,25	2.05	10 (40%)	26,38,38	1.88	6 (23%)
4	POP	A	400	2	6,8,8	1.43	0	12,13,13	0.96	1 (8%)
4	POP	C	400	2	6,8,8	1.51	1 (16%)	12,13,13	0.92	1 (8%)
3	IRP	A	300	2	25,25,25	1.96	9 (36%)	26,38,38	1.86	6 (23%)
3	IRP	C	300	2	25,25,25	2.04	9 (36%)	26,38,38	1.84	5 (19%)
3	IRP	B	300	2	25,25,25	2.17	9 (36%)	26,38,38	1.98	6 (23%)

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
4	POP	B	400	2	-	0/6/6/6	-
4	POP	D	400	2	-	0/6/6/6	-
3	IRP	D	300	2	-	3/10/26/26	0/3/3/3
4	POP	A	400	2	-	0/6/6/6	-
4	POP	C	400	2	-	0/6/6/6	-
3	IRP	A	300	2	-	3/10/26/26	0/3/3/3
3	IRP	C	300	2	-	3/10/26/26	0/3/3/3
3	IRP	B	300	2	-	3/10/26/26	0/3/3/3

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	300	IRP	C3'-C4'	-5.18	1.48	1.53
3	D	300	IRP	C3'-C4'	-3.92	1.49	1.53
3	C	300	IRP	C2-N3	3.92	1.37	1.30
3	D	300	IRP	C2-N3	3.90	1.37	1.30
3	A	300	IRP	C2-N3	3.85	1.37	1.30
3	B	300	IRP	C2-N3	3.84	1.37	1.30
3	B	300	IRP	C2-N1	3.67	1.41	1.35
3	C	300	IRP	C4'-N4'	-3.61	1.42	1.48
3	A	300	IRP	C3'-C4'	-3.47	1.50	1.53
3	C	300	IRP	C3'-C4'	-3.36	1.50	1.53
3	D	300	IRP	C2-N1	3.36	1.41	1.35
3	C	300	IRP	C1'-N4'	-3.33	1.41	1.46
3	D	300	IRP	C4'-N4'	-3.31	1.43	1.48
3	C	300	IRP	C2-N1	3.28	1.41	1.35
3	A	300	IRP	C4'-N4'	-3.25	1.43	1.48
3	A	300	IRP	C2-N1	3.12	1.41	1.35
3	B	300	IRP	C8-N7	-3.09	1.30	1.36
3	A	300	IRP	C8-N7	-3.06	1.30	1.36
3	B	300	IRP	C5-C4	3.03	1.41	1.38
3	D	300	IRP	C1'-N4'	-3.02	1.42	1.46
3	A	300	IRP	C1'-N4'	-3.02	1.42	1.46
3	B	300	IRP	C4'-N4'	-2.94	1.43	1.48
3	D	300	IRP	C8-N7	-2.92	1.30	1.36
3	C	300	IRP	C5-C4	2.84	1.41	1.38
3	B	300	IRP	C8-C9	2.81	1.41	1.37
3	B	300	IRP	C1'-N4'	-2.72	1.42	1.46
3	D	300	IRP	C5-C4	2.64	1.41	1.38
3	C	300	IRP	C8-N7	-2.57	1.31	1.36
3	C	300	IRP	C8-C9	2.48	1.40	1.37
3	C	300	IRP	P-O2P	-2.42	1.45	1.54
3	A	300	IRP	C8-C9	2.32	1.40	1.37
3	D	300	IRP	P-O2P	-2.23	1.46	1.54
4	B	400	POP	P2-O5	-2.22	1.46	1.54
3	B	300	IRP	P-O2P	-2.21	1.46	1.54
3	A	300	IRP	P-O2P	-2.14	1.46	1.54
3	D	300	IRP	C8-C9	2.12	1.40	1.37
4	C	400	POP	P2-O5	-2.12	1.46	1.54
3	D	300	IRP	C5'-C4'	-2.02	1.48	1.51
3	A	300	IRP	C5-C4	2.02	1.40	1.38

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	300	IRP	C9-C8-N7	4.98	115.86	108.70
3	D	300	IRP	C9-C8-N7	4.79	115.59	108.70
3	A	300	IRP	C9-C8-N7	4.61	115.33	108.70
3	C	300	IRP	C9-C8-N7	4.59	115.31	108.70
3	B	300	IRP	C8-N7-C5	-4.35	104.13	109.49
3	C	300	IRP	C8-N7-C5	-4.20	104.31	109.49
3	A	300	IRP	C8-N7-C5	-4.16	104.36	109.49
3	D	300	IRP	C8-N7-C5	-4.10	104.44	109.49
3	B	300	IRP	C4-C5-N7	3.80	111.10	105.57
3	D	300	IRP	C4-C5-N7	3.63	110.86	105.57
3	A	300	IRP	C4-C5-N7	3.62	110.85	105.57
3	C	300	IRP	C4-C5-N7	3.57	110.77	105.57
3	B	300	IRP	C5'-C4'-C3'	-2.89	108.78	113.75
3	B	300	IRP	N1-C2-N3	-2.81	122.26	125.50
3	D	300	IRP	N1-C2-N3	-2.81	122.27	125.50
3	C	300	IRP	N1-C2-N3	-2.79	122.28	125.50
3	A	300	IRP	N1-C2-N3	-2.74	122.34	125.50
3	B	300	IRP	O3'-C3'-C4'	-2.39	106.52	112.92
4	A	400	POP	O3-P1-O	2.39	112.64	104.64
3	A	300	IRP	O3'-C3'-C4'	-2.33	106.69	112.92
4	D	400	POP	O3-P1-O	2.32	112.41	104.64
3	D	300	IRP	C5'-C4'-C3'	-2.31	109.77	113.75
3	A	300	IRP	C5'-C4'-C3'	-2.30	109.79	113.75
3	C	300	IRP	O3'-C3'-C4'	-2.24	106.94	112.92
4	B	400	POP	O3-P1-O	2.20	112.01	104.64
3	D	300	IRP	O3'-C3'-C4'	-2.19	107.06	112.92
4	C	400	POP	O3-P1-O	2.17	111.93	104.64
4	B	400	POP	O5-P2-O	2.15	111.84	104.64

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	300	IRP	C5'-O5'-P-O1P
3	A	300	IRP	C5'-O5'-P-O2P
3	A	300	IRP	C5'-O5'-P-O3P
3	B	300	IRP	C5'-O5'-P-O2P
3	C	300	IRP	C5'-O5'-P-O1P
3	C	300	IRP	C5'-O5'-P-O2P
3	D	300	IRP	C5'-O5'-P-O2P
3	B	300	IRP	C5'-O5'-P-O3P
3	C	300	IRP	C5'-O5'-P-O3P
3	D	300	IRP	C5'-O5'-P-O3P

Continued on next page...

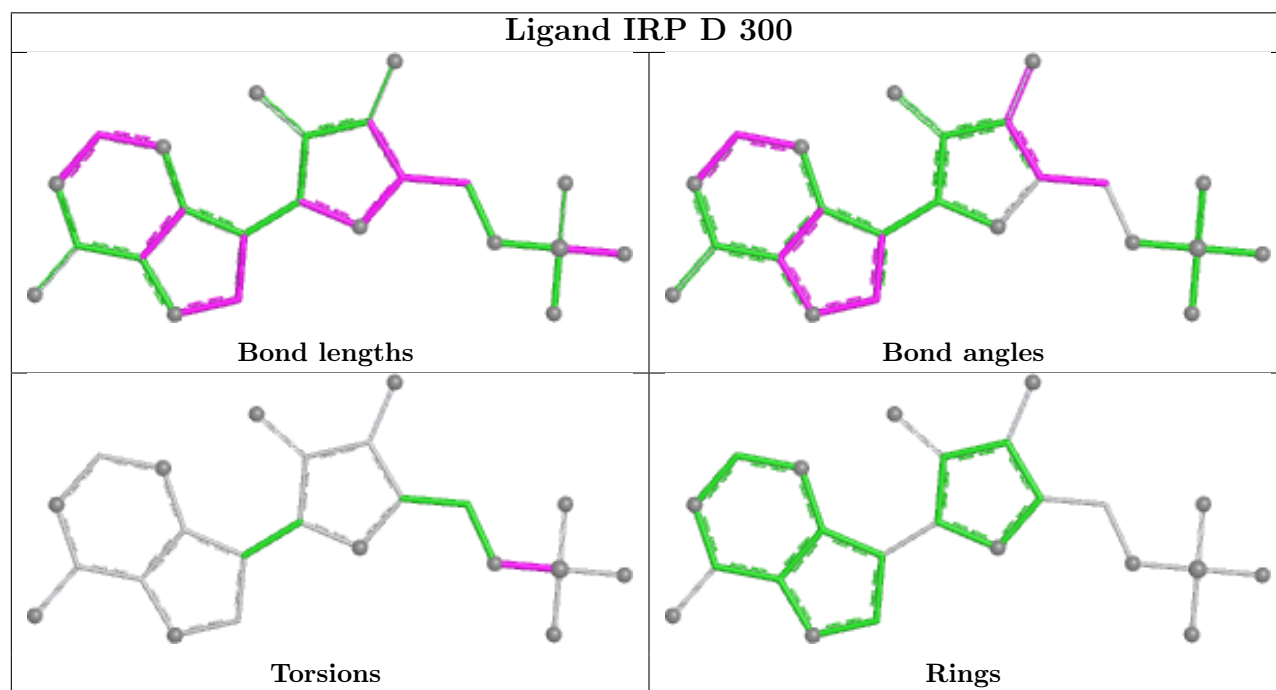
Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	300	IRP	C5'-O5'-P-O1P
3	D	300	IRP	C5'-O5'-P-O1P

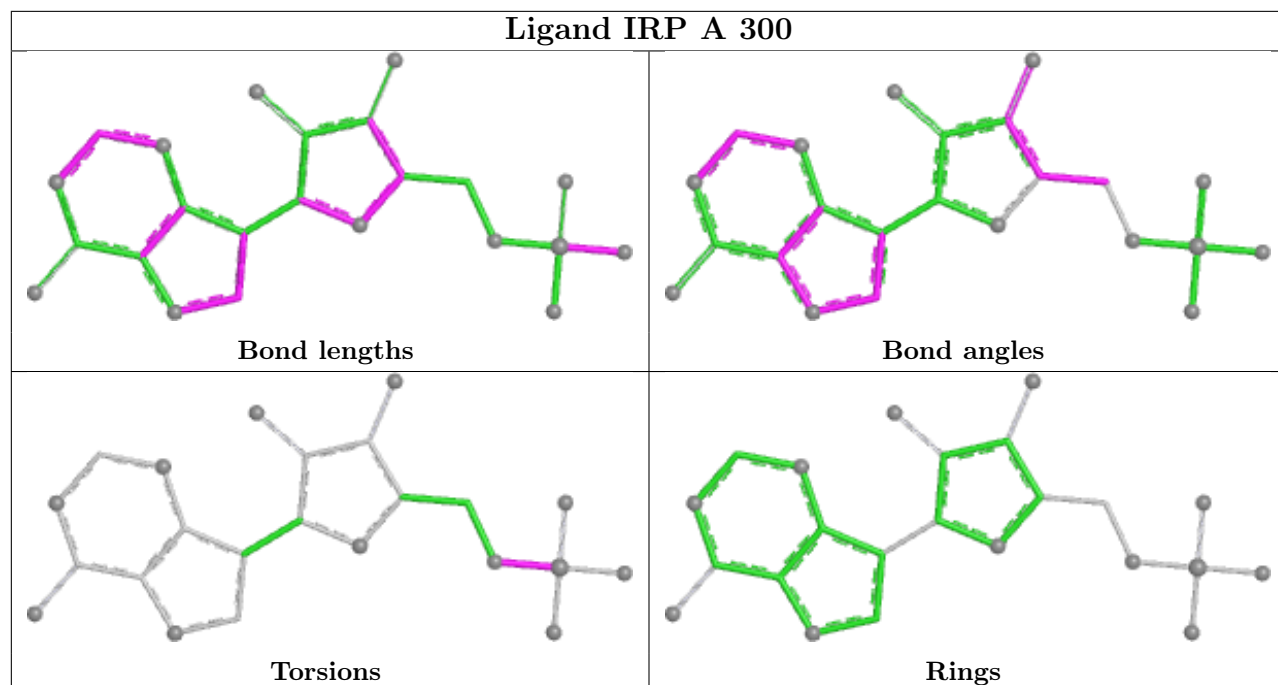
There are no ring outliers.

No monomer is involved in short contacts.

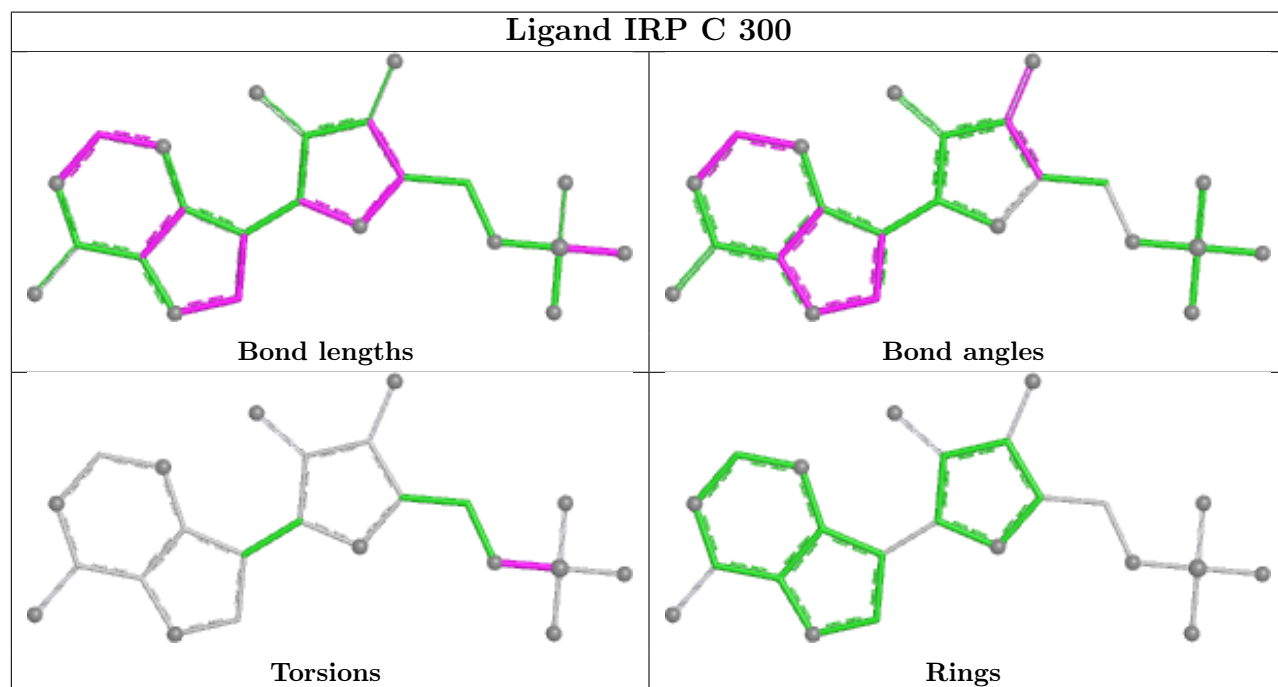
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

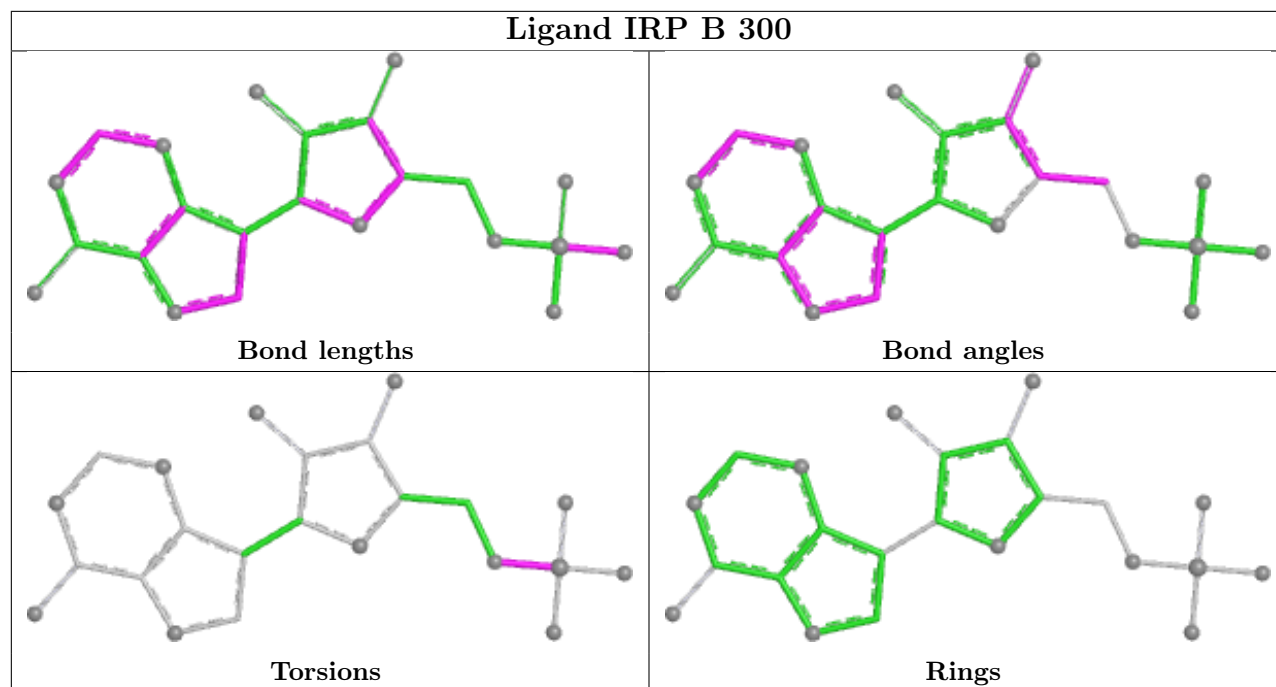


Ligand IRP A 300



Ligand IRP C 300





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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.