



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 08:22 am BST

PDB ID : 4IRU
Title : Crystal Structure of lepB GAP core in a transition state mimetic complex with Rab1A and ALF3
Authors : Mishra, A.K.; Delcampo, C.M.; Collins, R.E.; Roy, C.R.; Lambright, D.G.
Deposited on : 2013-01-15
Resolution : 3.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

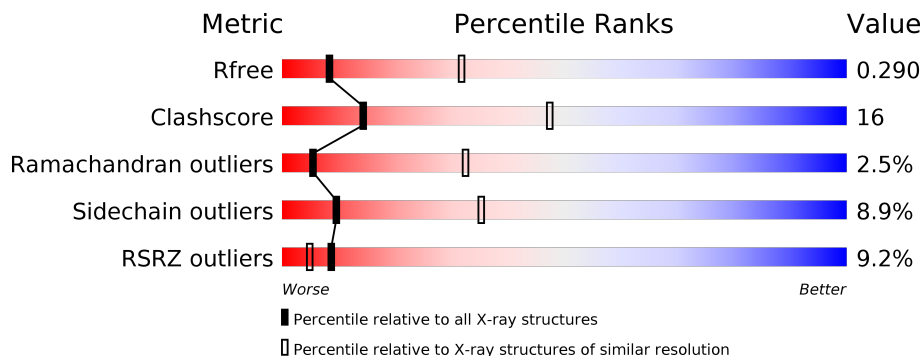
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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	299	
1	C	299	
1	E	299	
2	B	184	
2	D	184	
2	F	184	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	C	705	-	-	X	-
4	GOL	A	905	-	-	-	X

2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 11410 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 LepB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	296	2365	1526	389	443	4	3	0	0	0
1	C	296	2365	1526	389	443	4	3	0	0	0
1	E	295	2359	1523	388	441	4	3	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	325	SER	-	EXPRESSION TAG	UNP Q5ZSM7
C	325	SER	-	EXPRESSION TAG	UNP Q5ZSM7
E	325	SER	-	EXPRESSION TAG	UNP Q5ZSM7

- Molecule 2 is a protein called Ras-related protein Rab-1A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
2	B	170	1362	868	222	267	2	3	0	0	0
2	D	170	1362	868	222	267	2	3	0	0	0
2	F	170	1362	868	222	267	2	3	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

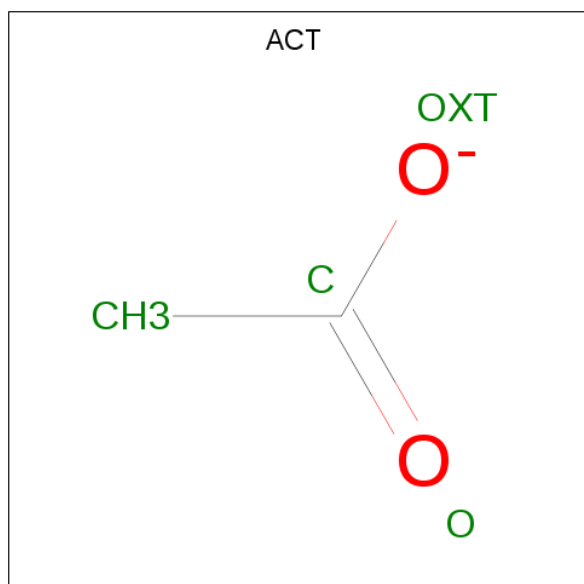
Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	MSE	-	EXPRESSION TAG	UNP P62820
B	-5	GLY	-	EXPRESSION TAG	UNP P62820
B	-4	HIS	-	EXPRESSION TAG	UNP P62820
B	-3	HIS	-	EXPRESSION TAG	UNP P62820
B	-2	HIS	-	EXPRESSION TAG	UNP P62820

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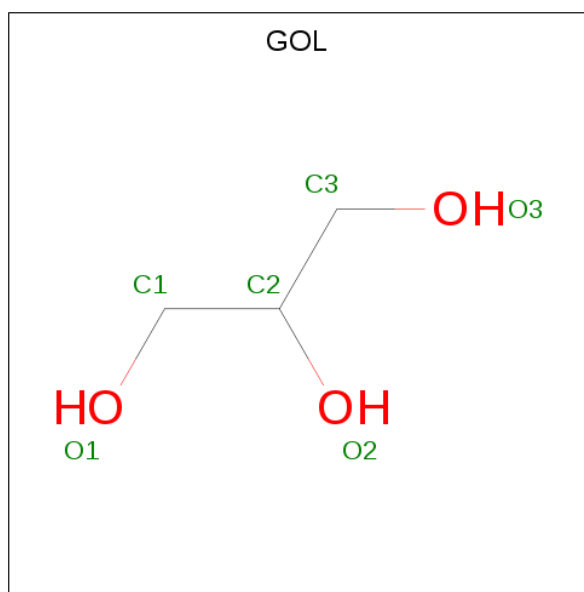
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	HIS	-	EXPRESSION TAG	UNP P62820
B	0	HIS	-	EXPRESSION TAG	UNP P62820
B	1	HIS	-	EXPRESSION TAG	UNP P62820
B	2	GLY	-	EXPRESSION TAG	UNP P62820
B	3	SER	-	EXPRESSION TAG	UNP P62820
D	-6	MSE	-	EXPRESSION TAG	UNP P62820
D	-5	GLY	-	EXPRESSION TAG	UNP P62820
D	-4	HIS	-	EXPRESSION TAG	UNP P62820
D	-3	HIS	-	EXPRESSION TAG	UNP P62820
D	-2	HIS	-	EXPRESSION TAG	UNP P62820
D	-1	HIS	-	EXPRESSION TAG	UNP P62820
D	0	HIS	-	EXPRESSION TAG	UNP P62820
D	1	HIS	-	EXPRESSION TAG	UNP P62820
D	2	GLY	-	EXPRESSION TAG	UNP P62820
D	3	SER	-	EXPRESSION TAG	UNP P62820
F	-6	MSE	-	EXPRESSION TAG	UNP P62820
F	-5	GLY	-	EXPRESSION TAG	UNP P62820
F	-4	HIS	-	EXPRESSION TAG	UNP P62820
F	-3	HIS	-	EXPRESSION TAG	UNP P62820
F	-2	HIS	-	EXPRESSION TAG	UNP P62820
F	-1	HIS	-	EXPRESSION TAG	UNP P62820
F	0	HIS	-	EXPRESSION TAG	UNP P62820
F	1	HIS	-	EXPRESSION TAG	UNP P62820
F	2	GLY	-	EXPRESSION TAG	UNP P62820
F	3	SER	-	EXPRESSION TAG	UNP P62820

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0

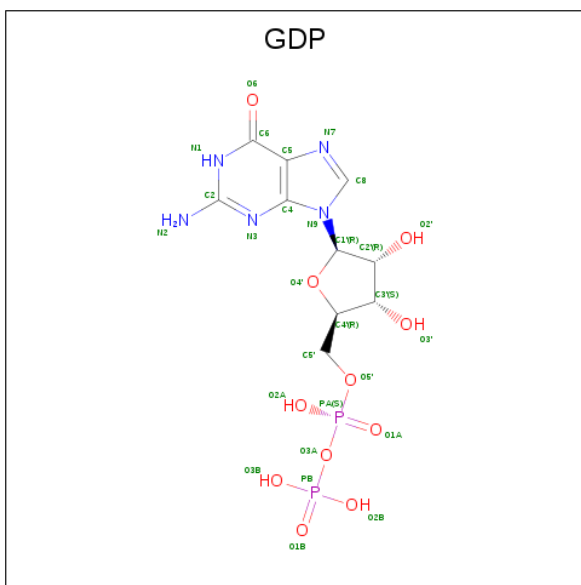
- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total K 1 1	0	0
5	A	4	Total K 4 4	0	0
5	C	1	Total K 1 1	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

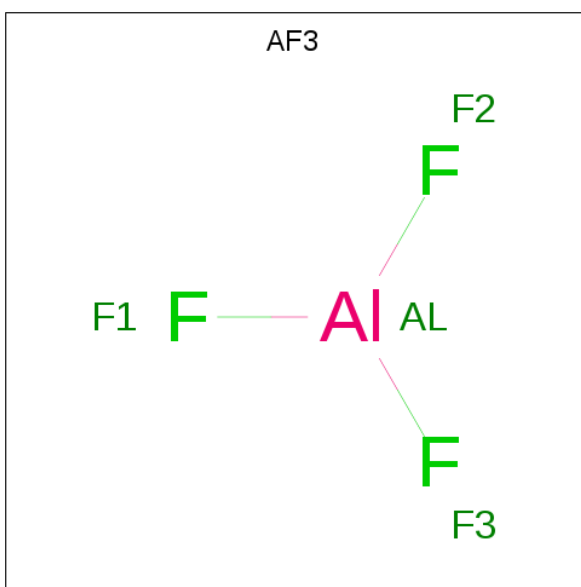
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Mg 1 1	0	0
6	D	1	Total Mg 1 1	0	0
6	F	1	Total Mg 1 1	0	0

- Molecule 7 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
7	B	1	28	10	5	11	2	0	0
7	D	1	28	10	5	11	2	0	0
7	F	1	28	10	5	11	2	0	0

- Molecule 8 is ALUMINUM FLUORIDE (three-letter code: AF3) (formula: AlF₃).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Al F		
8	B	1	4	1 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Al	F		
8	D	1	4	1	3	0	0
8	F	1	4	1	3	0	0

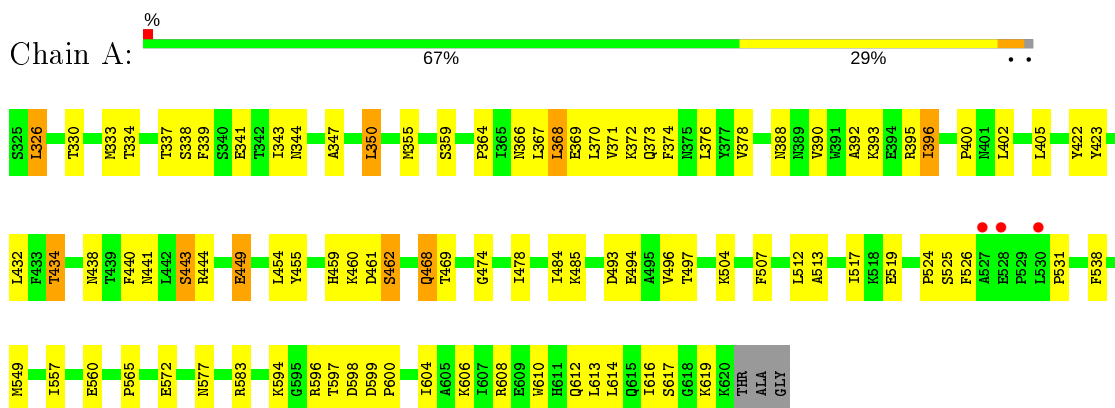
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	8	8	8	0	0
9	B	8	8	8	0	0
9	C	12	12	12	0	0
9	D	3	3	3	0	0
9	F	3	3	3	0	0

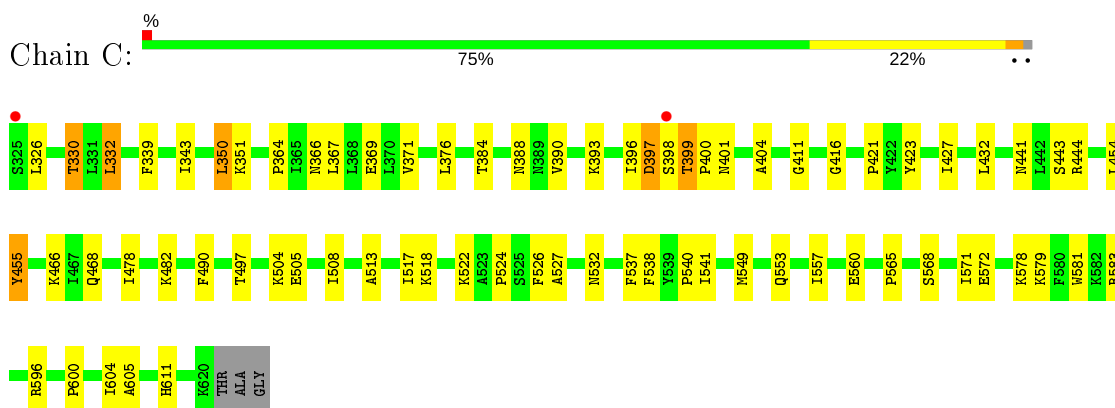
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

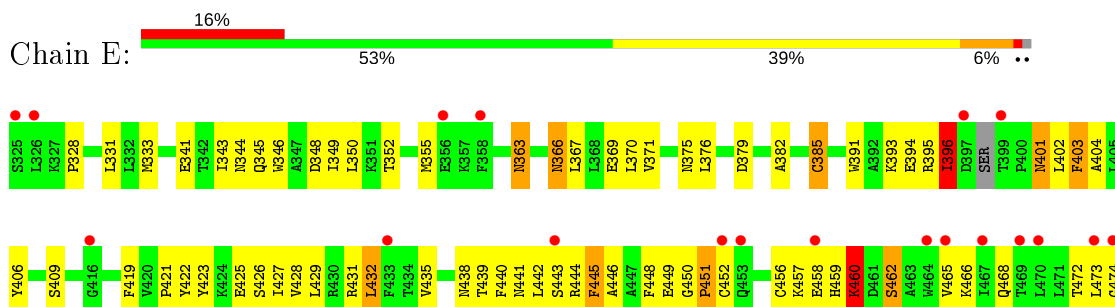
- Molecule 1: LepB



- Molecule 1: LepB



- Molecule 1: LepB



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	139.40Å 139.40Å 384.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.01 – 3.20 42.97 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (43.01-3.20) 100.0 (42.97-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.54	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.87 (at 3.19Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.230 , 0.288 0.230 , 0.290	Depositor DCC
R_{free} test set	1602 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	54.4	Xtrriage
Anisotropy	0.017	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	11410	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.16% 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: GDP, GOL, MG, K, ACT, AF3

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	0.55	0/2415	0.71	0/3262
1	C	0.55	0/2415	0.71	1/3262 (0.0%)
1	E	0.47	0/2408	0.67	1/3251 (0.0%)
2	B	0.46	0/1381	0.67	0/1859
2	D	0.42	0/1381	0.66	0/1859
2	F	0.45	0/1381	0.68	1/1859 (0.1%)
All	All	0.50	0/11381	0.69	3/15352 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	16	LEU	CA-CB-CG	5.26	127.41	115.30
1	C	332	LEU	CA-CB-CG	5.18	127.22	115.30
1	E	429	LEU	CA-CB-CG	5.06	126.94	115.30

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	2365	0	2378	50	0
1	C	2365	0	2378	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2359	0	2372	110	2
2	B	1362	0	1358	40	0
2	D	1362	0	1358	41	0
2	F	1362	0	1358	80	0
3	A	8	0	6	0	0
3	B	8	0	6	0	0
3	C	24	0	18	4	0
3	D	8	0	6	0	0
4	A	36	0	48	1	0
4	B	6	0	8	3	0
4	C	6	0	8	0	0
5	A	4	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
6	B	1	0	0	0	0
6	D	1	0	0	0	0
6	F	1	0	0	0	0
7	B	28	0	12	4	0
7	D	28	0	12	8	0
7	F	28	0	12	4	0
8	B	4	0	0	1	0
8	D	4	0	0	1	0
8	F	4	0	0	0	0
9	A	8	0	0	0	0
9	B	8	0	0	0	0
9	C	12	0	0	0	0
9	D	3	0	0	0	0
9	F	3	0	0	0	0
All	All	11410	0	11338	353	2

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 (353) 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)
2:B:53:ILE:HD11	2:B:166:MSE:SE	1.92	1.19
1:E:456:CYS:HA	1:E:465:VAL:HG22	1.44	1.00
1:E:479:ASN:O	1:E:483:ILE:HG12	1.62	0.99
1:C:393:LYS:HG3	1:C:524:PRO:HB3	1.46	0.97
2:F:118:ASN:HD21	2:F:175:ARG:HH21	1.15	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:508:ILE:HA	1:E:511:GLN:HG2	1.48	0.93
1:E:498:GLU:O	1:E:501:LYS:HB2	1.71	0.90
2:D:56:ASP:N	2:D:57:GLY:HA2	1.89	0.88
2:B:53:ILE:CD1	2:B:166:MSE:SE	2.73	0.86
1:E:457:LYS:HA	1:E:460:LYS:HE3	1.56	0.86
1:E:509:ALA:HA	1:E:512:LEU:HG	1.59	0.85
2:D:15:LEU:HD12	2:D:65:TRP:HB2	1.60	0.83
2:F:93:VAL:HG21	2:F:126:CYS:HA	1.62	0.82
1:C:366:ASN:ND2	1:C:369:GLU:HB2	1.95	0.82
1:E:428:VAL:HA	1:E:445:PHE:CE2	2.16	0.79
2:F:56:ASP:N	2:F:57:GLY:HA2	1.97	0.79
1:E:432:LEU:HD13	1:E:445:PHE:HD2	1.47	0.78
2:B:56:ASP:N	2:B:57:GLY:HA2	1.99	0.75
1:C:596:ARG:HB2	1:C:600:PRO:HG3	1.69	0.75
2:F:114:SER:HB2	2:F:117:VAL:HG23	1.69	0.75
1:E:403:PHE:HE2	1:E:428:VAL:HG11	1.53	0.74
1:C:423:TYR:OH	1:C:560:GLU:HG3	1.88	0.73
2:F:118:ASN:ND2	2:F:175:ARG:HH21	1.86	0.73
2:B:122:VAL:HG13	2:B:153:THR:CG2	2.19	0.73
1:E:475:ASN:HB3	2:F:44:ILE:HD13	1.72	0.72
2:B:15:LEU:HD12	2:B:65:TRP:HB2	1.72	0.72
1:A:326:LEU:HD12	1:A:326:LEU:H	1.55	0.71
1:E:508:ILE:HA	1:E:511:GLN:CG	2.20	0.71
1:C:366:ASN:HD21	1:C:369:GLU:HB2	1.56	0.70
2:D:30:ARG:O	2:D:34:ASP:HA	1.90	0.70
2:F:12:PHE:HB2	2:F:62:LEU:CD2	2.20	0.70
1:C:513:ALA:O	1:C:517:ILE:HD13	1.91	0.70
2:D:13:LYS:H	2:D:85:HIS:HD2	1.40	0.70
2:F:56:ASP:H	2:F:57:GLY:HA2	1.53	0.70
1:E:402:LEU:HD12	1:E:425:GLU:OE2	1.91	0.69
1:C:427:ILE:HD12	1:C:537:PHE:HD1	1.57	0.69
1:E:462:SER:O	1:E:466:LYS:HG2	1.93	0.68
1:E:435:VAL:HG13	1:E:440:PHE:O	1.94	0.68
1:A:549:MSE:O	1:A:583:ARG:NH1	2.26	0.68
1:E:343:ILE:HG23	1:E:507:PHE:CD1	2.28	0.68
2:F:10:TYR:HB2	2:F:60:ILE:HG12	1.75	0.67
1:E:539:TYR:HB3	1:E:540:PRO:CD	2.22	0.67
2:F:154:SER:HB3	2:F:159:THR:HB	1.77	0.67
1:C:540:PRO:HA	3:C:705:ACT:C	2.24	0.67
1:E:441:ASN:HB2	2:F:41:ILE:HG23	1.78	0.66
1:A:350:LEU:HD12	1:A:504:LYS:HB2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:535:SER:HB2	1:E:570:LEU:HD22	1.78	0.65
1:E:393:LYS:HB3	1:E:394:GLU:OE2	1.96	0.65
1:A:600:PRO:O	1:A:604:ILE:HG12	1.97	0.65
2:F:168:MSE:HG3	2:F:172:ILE:HD11	1.79	0.65
2:F:26:CYS:HG	2:F:36:TYR:HE1	1.38	0.65
1:C:366:ASN:ND2	1:C:369:GLU:CB	2.60	0.64
2:B:80:TYR:CD2	4:B:206:GOL:H32	2.32	0.64
1:A:423:TYR:OH	1:A:560:GLU:HG3	1.97	0.64
2:D:13:LYS:H	2:D:85:HIS:CD2	2.15	0.64
2:B:31:PHE:CE2	2:B:165:PHE:HB2	2.32	0.64
1:E:401:ASN:ND2	1:E:421:PRO:O	2.25	0.64
1:C:330:THR:OG1	1:C:364:PRO:HG2	1.99	0.63
2:F:12:PHE:HD1	2:F:85:HIS:HD2	1.45	0.63
2:B:150:PHE:O	2:B:151:LEU:HD12	1.99	0.63
2:D:135:ASP:O	2:D:138:THR:HG23	1.98	0.63
1:E:427:ILE:HG13	1:E:537:PHE:HA	1.80	0.62
2:F:55:LEU:O	2:F:56:ASP:HB2	1.99	0.62
2:B:142:PHE:O	2:B:145:SER:HB3	1.98	0.62
2:D:128:LEU:HD13	7:D:202:GDP:HN21	1.65	0.62
2:D:12:PHE:HA	2:D:85:HIS:CD2	2.35	0.61
1:E:555:ALA:O	1:E:559:LEU:HG	1.99	0.61
1:A:468:GLN:HG3	1:A:469:THR:N	2.15	0.61
2:D:12:PHE:HA	2:D:85:HIS:HD2	1.65	0.61
1:E:432:LEU:HD13	1:E:445:PHE:CD2	2.33	0.61
1:E:571:ILE:HA	1:E:574:ILE:HG13	1.81	0.61
1:E:578:LYS:HA	1:E:581:TRP:HB3	1.83	0.61
1:A:449:GLU:OE2	2:B:70:GLN:HG2	2.01	0.60
1:E:404:ALA:HA	1:E:419:PHE:CE2	2.36	0.60
1:E:561:GLU:HG3	1:E:571:ILE:HB	1.84	0.60
2:F:35:THR:HG22	2:F:36:TYR:N	2.16	0.60
2:B:80:TYR:HD2	4:B:206:GOL:H32	1.65	0.60
1:C:388:ASN:O	1:C:524:PRO:HD2	2.02	0.59
1:E:428:VAL:HA	1:E:445:PHE:HE2	1.64	0.59
1:E:456:CYS:HA	1:E:465:VAL:CG2	2.26	0.59
2:F:26:CYS:O	2:F:29:LEU:HB3	2.02	0.59
2:D:30:ARG:HG3	2:D:30:ARG:HH11	1.66	0.59
2:F:12:PHE:HB2	2:F:62:LEU:HD22	1.85	0.59
2:B:111:ARG:HD2	2:B:112:TYR:CZ	2.38	0.59
1:E:492:ILE:HD11	2:F:50:ILE:HD11	1.85	0.58
2:F:37:THR:O	2:F:37:THR:HG23	2.03	0.58
2:B:135:ASP:HB3	2:B:137:THR:HG23	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:399:THR:HB	1:C:404:ALA:HB3	1.84	0.58
1:E:406:TYR:HB2	1:E:451:PRO:HB3	1.86	0.58
2:F:104:GLN:O	2:F:108:GLU:HG2	2.03	0.58
2:B:114:SER:HB2	2:B:117:VAL:HG23	1.86	0.58
2:D:38:GLU:HA	2:D:38:GLU:OE2	2.04	0.58
2:F:77:THR:HG22	2:F:81:TYR:CE1	2.38	0.58
1:A:355:MSE:O	1:A:355:MSE:HE3	2.03	0.58
1:E:561:GLU:O	1:E:563:ASN:N	2.37	0.57
2:D:19:ASP:O	2:D:24:LYS:NZ	2.37	0.57
2:F:35:THR:CG2	2:F:36:TYR:N	2.67	0.57
2:F:67:THR:HB	2:F:77:THR:HG23	1.87	0.57
1:A:493:ASP:O	1:A:497:THR:HG22	2.04	0.57
2:D:128:LEU:CD1	7:D:202:GDP:N2	2.67	0.57
2:B:122:VAL:HG13	2:B:153:THR:HG21	1.86	0.57
2:F:77:THR:HG22	2:F:81:TYR:HE1	1.69	0.57
1:E:503:LEU:HG	1:E:507:PHE:CE2	2.40	0.56
2:B:67:THR:HB	2:B:77:THR:HG22	1.87	0.56
1:E:479:ASN:O	1:E:483:ILE:CG1	2.47	0.56
1:E:539:TYR:HB3	1:E:540:PRO:HD2	1.87	0.56
2:F:26:CYS:HB2	7:F:201:GDP:O2A	2.06	0.56
2:B:53:ILE:HG22	2:B:60:ILE:HB	1.88	0.56
1:E:591:GLY:O	1:E:594:LYS:HB2	2.06	0.56
2:F:120:LEU:HD21	2:F:164:SER:HB3	1.88	0.56
2:F:22:VAL:HG22	2:F:92:ASP:HB2	1.88	0.56
2:F:129:THR:HG22	2:F:132:LYS:HD2	1.89	0.55
1:C:398:SER:O	1:C:399:THR:C	2.44	0.55
2:F:25:SER:N	7:F:201:GDP:O3B	2.39	0.55
1:E:591:GLY:O	1:E:594:LYS:CB	2.55	0.55
1:E:509:ALA:CA	1:E:512:LEU:HG	2.35	0.55
2:D:33:ASP:HB2	2:D:35:THR:HG22	1.89	0.55
2:B:113:ALA:HB1	2:B:117:VAL:HG21	1.89	0.55
1:C:549:MSE:O	1:C:583:ARG:NH1	2.36	0.54
1:E:404:ALA:HA	1:E:419:PHE:HE2	1.71	0.54
1:A:368:LEU:HD12	1:A:372:LYS:HD3	1.89	0.54
2:F:22:VAL:HG12	2:F:90:VAL:HG12	1.89	0.54
1:C:351:LYS:HA	1:C:504:LYS:HE3	1.90	0.54
1:E:444:ARG:HD2	2:F:40:TYR:HB3	1.89	0.54
2:F:20:SER:OG	2:F:70:GLN:NE2	2.41	0.54
1:E:444:ARG:O	1:E:446:ALA:N	2.42	0.53
1:A:366:ASN:OD1	1:A:369:GLU:HB2	2.08	0.53
2:F:23:GLY:HA3	2:F:124:ASN:OD1	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:29:LEU:HD21	2:D:35:THR:HG23	1.90	0.53
1:E:403:PHE:CE2	1:E:428:VAL:HG11	2.37	0.53
1:A:513:ALA:O	1:A:517:ILE:HD13	2.09	0.53
1:E:343:ILE:HG23	1:E:507:PHE:HD1	1.72	0.53
1:E:366:ASN:OD1	1:E:369:GLU:HB2	2.09	0.52
1:A:400:PRO:HB3	1:A:422:TYR:CD1	2.43	0.52
2:B:175:ARG:O	2:B:175:ARG:HG2	2.08	0.52
2:F:35:THR:CG2	2:F:36:TYR:H	2.22	0.52
1:E:393:LYS:HE2	1:E:394:GLU:HG3	1.90	0.52
2:F:170:ALA:HA	2:F:173:LYS:HB3	1.91	0.52
1:E:406:TYR:O	1:E:451:PRO:HG3	2.09	0.52
2:F:156:LYS:HB2	7:F:201:GDP:N1	2.24	0.52
2:D:128:LEU:HD13	7:D:202:GDP:N2	2.24	0.52
1:E:472:THR:HG22	1:E:473:LEU:HG	1.92	0.52
2:F:109:ILE:HG23	2:F:113:ALA:HB3	1.92	0.52
2:D:111:ARG:HD2	2:D:112:TYR:CZ	2.44	0.52
2:F:113:ALA:HB1	2:F:117:VAL:HG21	1.91	0.51
1:E:331:LEU:HB3	1:E:346:TRP:CE2	2.45	0.51
1:E:441:ASN:HD22	2:F:44:ILE:H	1.57	0.51
1:A:504:LYS:O	1:A:507:PHE:HB2	2.10	0.51
1:E:517:ILE:HG22	1:E:520:SER:HB2	1.91	0.51
2:F:17:ILE:HD11	2:F:81:TYR:CE2	2.45	0.51
1:A:326:LEU:HD13	1:A:359:SER:HB2	1.92	0.51
2:D:74:ARG:O	2:D:78:SER:HB3	2.10	0.51
2:D:21:GLY:N	7:D:202:GDP:O1B	2.43	0.51
1:E:348:ASP:O	1:E:352:THR:HG22	2.10	0.51
2:F:55:LEU:HD11	2:F:166:MSE:SE	2.60	0.51
1:E:509:ALA:HA	1:E:512:LEU:CG	2.34	0.51
1:E:375:ASN:HD21	1:E:435:VAL:HB	1.75	0.51
1:A:538:PHE:CE2	1:A:557:ILE:HG23	2.46	0.51
1:E:606:LYS:O	1:E:610:TRP:CD1	2.64	0.50
2:F:168:MSE:HG3	2:F:172:ILE:CD1	2.40	0.50
2:D:120:LEU:HD12	2:D:168:MSE:HB2	1.92	0.50
2:D:29:LEU:CD2	2:D:35:THR:HG23	2.41	0.50
1:C:427:ILE:CD1	1:C:537:PHE:HD1	2.23	0.50
2:F:46:VAL:O	2:F:47:ASP:HB2	2.11	0.50
2:B:125:LYS:HG2	7:B:202:GDP:C5	2.46	0.50
1:E:367:LEU:O	1:E:370:LEU:HB3	2.12	0.50
1:E:565:PRO:C	1:E:566:LYS:HG2	2.31	0.50
1:E:363:ASN:N	1:E:363:ASN:OD1	2.45	0.50
2:F:91:TYR:HE2	2:F:150:PHE:HE1	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:ARG:HB3	1:A:598:ASP:OD1	2.12	0.49
2:F:155:ALA:HB3	7:F:201:GDP:O6	2.12	0.49
1:A:338:SER:HA	1:A:373:GLN:OE1	2.13	0.49
2:B:116:ASN:HD22	2:B:175:ARG:HE	1.60	0.49
1:E:493:ASP:O	1:E:497:THR:HG22	2.12	0.49
2:F:28:LEU:HD22	2:F:66:ASP:HB3	1.94	0.49
2:F:53:ILE:HD11	2:F:166:MSE:SE	2.62	0.49
1:A:577:ASN:C	1:A:577:ASN:OD1	2.51	0.49
2:B:67:THR:HB	2:B:77:THR:CG2	2.42	0.49
1:E:385:CYS:HB3	1:E:391:TRP:CZ2	2.48	0.49
2:D:125:LYS:HG2	7:D:202:GDP:C6	2.48	0.49
2:F:30:ARG:HH21	2:F:36:TYR:HB2	1.78	0.48
2:F:25:SER:OG	2:F:66:ASP:OD2	2.31	0.48
1:A:333:MSE:HE1	1:A:370:LEU:HA	1.94	0.48
2:D:113:ALA:HB1	2:D:117:VAL:HG21	1.95	0.48
1:E:439:THR:O	1:E:440:PHE:HB2	2.13	0.48
2:D:137:THR:OG1	2:D:138:THR:N	2.47	0.48
1:E:382:ALA:HB1	1:E:426:SER:HB3	1.95	0.48
2:F:30:ARG:HH11	2:F:158:ALA:HB2	1.79	0.48
1:A:344:ASN:O	1:A:347:ALA:HB3	2.14	0.48
2:F:63:GLN:C	2:F:64:ILE:HG13	2.33	0.48
2:D:43:THR:HB	8:D:203:AF3:F1	2.04	0.48
2:F:25:SER:OG	2:F:43:THR:OG1	2.25	0.48
2:F:81:TYR:O	2:F:84:ALA:HB3	2.12	0.48
1:A:378:VAL:HG11	1:A:434:THR:HG23	1.95	0.47
1:C:532:ASN:HD21	3:C:705:ACT:H3	1.79	0.47
1:A:371:VAL:HG21	1:A:440:PHE:CD1	2.49	0.47
2:F:33:ASP:O	2:F:34:ASP:HB2	2.15	0.47
1:C:367:LEU:HD11	1:C:482:LYS:HA	1.97	0.47
2:B:43:THR:HB	8:B:203:AF3:F1	2.04	0.47
2:F:47:ASP:O	2:F:65:TRP:CE3	2.68	0.47
1:A:330:THR:OG1	1:A:364:PRO:HG2	2.14	0.47
1:A:484:ILE:HG23	1:A:496:VAL:HG13	1.97	0.47
2:F:102:VAL:HG22	2:F:121:LEU:HD11	1.97	0.47
1:A:455:TYR:C	1:A:455:TYR:CD1	2.88	0.47
2:F:158:ALA:HA	2:F:161:VAL:HG22	1.97	0.47
2:D:58:LYS:HG3	2:D:173:LYS:NZ	2.31	0.46
1:E:428:VAL:HA	1:E:445:PHE:CZ	2.49	0.46
1:E:474:GLY:HA2	1:E:477:ILE:HD12	1.97	0.46
2:F:143:ALA:HB1	2:F:150:PHE:HB2	1.96	0.46
1:A:444:ARG:NH2	7:B:202:GDP:O1B	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:540:PRO:HA	3:C:705:ACT:O	2.15	0.46
1:E:466:LYS:HB3	1:E:517:ILE:HG12	1.97	0.46
1:E:562:LEU:HB3	1:E:603:LYS:HE2	1.97	0.46
2:F:116:ASN:HD22	2:F:175:ARG:HD2	1.81	0.46
2:F:157:ASN:O	2:F:158:ALA:HB3	2.15	0.46
1:C:396:ILE:HG13	1:C:397:ASP:OD1	2.15	0.46
2:D:55:LEU:O	2:D:56:ASP:HB2	2.15	0.46
1:E:450:GLY:O	1:E:452:CYS:N	2.48	0.46
2:F:124:ASN:HD21	2:F:155:ALA:H	1.63	0.46
2:F:23:GLY:O	2:F:24:LYS:C	2.54	0.46
1:E:350:LEU:HD22	1:E:355:MSE:SE	2.66	0.46
1:E:431:ARG:HB2	1:E:445:PHE:CG	2.51	0.46
1:E:456:CYS:HB3	1:E:465:VAL:HG13	1.96	0.46
1:A:334:THR:HB	1:A:337:THR:HG23	1.97	0.46
1:A:388:ASN:O	1:A:524:PRO:HD2	2.16	0.46
1:A:606:LYS:HD3	1:A:610:TRP:CZ2	2.51	0.46
1:C:400:PRO:HB2	1:C:421:PRO:O	2.15	0.46
1:E:341:GLU:O	1:E:345:GLN:HG3	2.16	0.46
1:A:441:ASN:HA	2:B:44:ILE:HG13	1.97	0.46
1:E:497:THR:HA	1:E:500:LEU:HD12	1.97	0.46
1:C:455:TYR:CD1	1:C:455:TYR:C	2.88	0.46
1:E:352:THR:HG23	1:E:352:THR:O	2.16	0.46
1:A:459:HIS:HB3	1:A:462:SER:HB3	1.97	0.46
1:C:416:GLY:O	1:C:596:ARG:NH1	2.45	0.45
1:E:532:ASN:HD21	1:E:540:PRO:HD3	1.81	0.45
1:C:581:TRP:CE2	1:C:611:HIS:CD2	3.04	0.45
1:E:444:ARG:C	1:E:446:ALA:N	2.70	0.45
1:E:403:PHE:O	1:E:419:PHE:CZ	2.70	0.45
2:F:27:LEU:HD21	2:F:124:ASN:ND2	2.32	0.45
2:B:128:LEU:HD11	7:B:202:GDP:N2	2.31	0.45
2:D:11:LEU:HD13	2:D:61:LYS:HD3	1.98	0.45
2:B:157:ASN:O	2:B:158:ALA:HB3	2.16	0.45
1:C:339:PHE:O	1:C:343:ILE:HG12	2.17	0.45
1:E:562:LEU:HB3	1:E:603:LYS:CE	2.47	0.45
1:A:400:PRO:HB3	1:A:422:TYR:CE1	2.51	0.45
1:A:460:LYS:O	1:A:461:ASP:HB2	2.17	0.45
1:E:404:ALA:HB2	1:E:421:PRO:HB3	1.98	0.45
2:D:118:ASN:HD22	2:D:172:ILE:HG12	1.81	0.45
2:D:85:HIS:HB3	2:D:172:ILE:HD13	1.99	0.45
1:E:331:LEU:HB3	1:E:346:TRP:NE1	2.31	0.45
1:C:441:ASN:HA	2:D:44:ILE:HG13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:505:GLU:HA	1:C:508:ILE:HD12	1.99	0.45
1:A:443:SER:HB2	4:A:907:GOL:H2	1.99	0.45
2:B:128:LEU:CD1	7:B:202:GDP:N2	2.79	0.44
1:E:466:LYS:CB	1:E:517:ILE:HG12	2.47	0.44
1:E:602:GLY:O	1:E:606:LYS:HB2	2.16	0.44
1:E:616:ILE:HG13	1:E:616:ILE:H	1.67	0.44
2:D:158:ALA:O	2:D:159:THR:C	2.55	0.44
1:E:428:VAL:HG13	1:E:445:PHE:HE2	1.83	0.44
1:E:572:GLU:OE2	1:E:576:SER:OG	2.36	0.44
2:D:157:ASN:O	2:D:158:ALA:HB3	2.18	0.44
1:E:343:ILE:HG23	1:E:507:PHE:CE1	2.52	0.44
2:B:50:ILE:HA	2:B:62:LEU:O	2.19	0.43
1:C:423:TYR:OH	1:C:560:GLU:CG	2.62	0.43
1:E:371:VAL:HG21	1:E:440:PHE:CD1	2.53	0.43
1:E:422:TYR:HD2	1:E:549:MSE:HE1	1.83	0.43
2:D:17:ILE:HD11	2:D:89:VAL:HG22	2.00	0.43
1:C:454:LEU:HD23	1:C:454:LEU:HA	1.72	0.43
1:E:403:PHE:N	1:E:403:PHE:CD1	2.85	0.43
1:E:468:GLN:HG2	1:E:468:GLN:O	2.18	0.43
2:F:78:SER:HA	2:F:81:TYR:CD1	2.53	0.43
1:A:350:LEU:HD22	1:A:350:LEU:HA	1.65	0.43
1:A:614:LEU:HD23	1:A:614:LEU:HA	1.82	0.43
2:B:63:GLN:HE21	2:B:65:TRP:HE1	1.65	0.43
2:B:19:ASP:O	2:B:24:LYS:NZ	2.51	0.43
1:E:472:THR:O	2:F:73:PHE:HE1	2.02	0.43
1:A:390:VAL:O	1:A:393:LYS:HB2	2.19	0.43
2:D:95:ASP:OD2	2:D:98:SER:HB3	2.18	0.43
2:F:153:THR:HB	2:F:161:VAL:HG12	2.00	0.43
1:C:568:SER:O	1:C:571:ILE:HG22	2.19	0.43
1:E:333:MSE:HB2	1:E:333:MSE:HE3	1.97	0.43
1:E:385:CYS:HB3	1:E:391:TRP:CE2	2.54	0.43
1:E:441:ASN:HB2	2:F:41:ILE:CG2	2.48	0.43
1:E:441:ASN:ND2	2:F:43:THR:HA	2.34	0.43
1:C:596:ARG:CB	1:C:600:PRO:HG3	2.42	0.42
2:F:91:TYR:CE1	2:F:134:VAL:HG11	2.53	0.42
2:B:17:ILE:HD11	2:B:89:VAL:HG22	2.01	0.42
1:C:541:ILE:H	3:C:705:ACT:C	2.30	0.42
1:A:367:LEU:HA	1:A:367:LEU:HD23	1.79	0.42
2:D:13:LYS:N	2:D:85:HIS:HD2	2.12	0.42
1:E:495:ALA:HA	1:E:498:GLU:HB2	2.01	0.42
2:B:116:ASN:N	2:B:116:ASN:OD1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:367:LEU:HD23	1:C:367:LEU:HA	1.95	0.42
1:C:399:THR:HA	1:C:400:PRO:HD3	1.91	0.42
2:F:16:LEU:HB2	2:F:66:ASP:HA	2.00	0.42
1:A:367:LEU:O	1:A:368:LEU:C	2.58	0.42
2:B:135:ASP:O	2:B:136:TYR:C	2.58	0.42
2:B:30:ARG:O	2:B:34:ASP:HA	2.20	0.42
2:F:153:THR:HG22	2:F:160:ASN:O	2.20	0.42
2:D:168:MSE:O	2:D:172:ILE:HG13	2.20	0.41
1:E:423:TYR:CD2	1:E:448:PHE:CZ	3.07	0.41
1:E:538:PHE:CE1	1:E:557:ILE:HG23	2.55	0.41
2:F:46:VAL:HG12	2:F:67:THR:HA	2.02	0.41
2:B:175:ARG:O	2:B:175:ARG:CG	2.68	0.41
1:C:350:LEU:HA	1:C:350:LEU:HD23	1.84	0.41
2:F:109:ILE:HG21	2:F:119:LYS:HE2	2.02	0.41
1:E:558:CYS:C	1:E:560:GLU:N	2.74	0.41
1:A:374:PHE:CE1	1:A:474:GLY:HA3	2.54	0.41
1:C:444:ARG:NH1	7:D:202:GDP:O1B	2.49	0.41
1:E:331:LEU:HD13	1:E:346:TRP:CD2	2.55	0.41
1:E:457:LYS:HA	1:E:460:LYS:CE	2.38	0.41
1:A:326:LEU:N	1:A:326:LEU:HD12	2.30	0.41
1:E:435:VAL:HA	1:E:441:ASN:O	2.20	0.41
1:E:599:ASP:CG	1:E:602:GLY:HA3	2.40	0.41
1:A:392:ALA:HA	1:A:395:ARG:HD2	2.03	0.41
1:E:459:HIS:O	1:E:465:VAL:HG21	2.21	0.41
1:A:341:GLU:HA	1:A:344:ASN:HB3	2.03	0.41
2:B:44:ILE:HG22	2:B:45:GLY:N	2.36	0.41
1:C:371:VAL:HG22	1:C:478:ILE:HD13	2.03	0.41
1:C:604:ILE:O	1:C:605:ALA:C	2.58	0.41
2:D:125:LYS:HG2	7:D:202:GDP:C5	2.56	0.41
2:B:124:ASN:HA	2:B:153:THR:O	2.21	0.41
1:E:422:TYR:CD2	1:E:549:MSE:HE1	2.56	0.41
1:E:561:GLU:CB	1:E:571:ILE:HB	2.51	0.41
2:F:125:LYS:HB3	2:F:128:LEU:HD13	2.03	0.41
2:F:12:PHE:HB2	2:F:62:LEU:HD21	2.00	0.41
1:C:466:LYS:O	1:C:517:ILE:HD11	2.21	0.41
2:D:74:ARG:HA	2:D:74:ARG:HD3	1.93	0.41
2:F:168:MSE:HE2	2:F:168:MSE:HB2	2.00	0.41
1:C:401:ASN:OD1	1:C:401:ASN:C	2.59	0.41
1:C:490:PHE:N	1:C:490:PHE:CD1	2.89	0.41
1:E:589:GLU:O	1:E:590:SER:C	2.59	0.41
2:F:172:ILE:HG23	2:F:175:ARG:HH22	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:128:LEU:HD11	7:D:202:GDP:N2	2.35	0.40
1:E:561:GLU:O	1:E:564:SER:N	2.27	0.40
2:B:13:LYS:HD2	4:B:206:GOL:O2	2.22	0.40
1:A:371:VAL:HG22	1:A:478:ILE:HD13	2.03	0.40
1:A:608:ARG:O	1:A:612:GLN:HG3	2.21	0.40
1:A:613:LEU:O	1:A:616:ILE:HB	2.21	0.40
2:B:76:ILE:O	2:B:77:THR:C	2.59	0.40
1:C:411:GLY:HA2	1:C:553:GLN:HE21	1.87	0.40
1:C:390:VAL:O	1:C:393:LYS:HB2	2.21	0.40
1:C:538:PHE:CE2	1:C:557:ILE:HG23	2.57	0.40
2:D:132:LYS:HE2	2:D:134:VAL:O	2.22	0.40
1:E:343:ILE:CG2	1:E:507:PHE:HD1	2.33	0.40
1:E:442:LEU:HD11	2:F:72:ARG:HH22	1.86	0.40
1:E:423:TYR:HE1	1:E:560:GLU:HG2	1.86	0.40
1:A:339:PHE:O	1:A:343:ILE:HG12	2.22	0.40
1:A:371:VAL:HG21	1:A:440:PHE:HD1	1.85	0.40
1:A:599:ASP:O	1:A:600:PRO:C	2.60	0.40
2:B:74:ARG:O	2:B:75:THR:C	2.60	0.40
1:E:558:CYS:O	1:E:560:GLU:N	2.54	0.40
2:F:128:LEU:O	2:F:132:LYS:HB2	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:395:ARG:O	1:E:395:ARG:O[6_555]	1.49	0.71
1:E:396:ILE:O	1:E:396:ILE:O[6_555]	2.17	0.03

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	294/299 (98%)	267 (91%)	23 (8%)	4 (1%)	11	46
1	C	294/299 (98%)	273 (93%)	19 (6%)	2 (1%)	22	61
1	E	291/299 (97%)	231 (79%)	44 (15%)	16 (6%)	2	14
2	B	168/184 (91%)	150 (89%)	16 (10%)	2 (1%)	13	49
2	D	168/184 (91%)	149 (89%)	16 (10%)	3 (2%)	8	41
2	F	168/184 (91%)	132 (79%)	28 (17%)	8 (5%)	2	17
All	All	1383/1449 (95%)	1202 (87%)	146 (11%)	35 (2%)	5	32

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	445	PHE
1	E	596	ARG
1	E	598	ASP
2	F	24	LYS
2	F	46	VAL
2	F	47	ASP
2	F	56	ASP
1	E	451	PRO
1	E	539	TYR
1	E	562	LEU
1	E	600	PRO
2	F	34	ASP
1	A	402	LEU
1	A	531	PRO
1	A	565	PRO
2	B	137	THR
2	D	56	ASP
1	E	619	LYS
2	F	45	GLY
2	B	159	THR
1	C	527	ALA
2	D	19	ASP
2	D	130	THR
1	E	409	SER
1	E	460	LYS
1	E	501	LYS
2	F	35	THR
2	F	168	MSE
1	A	396	ILE
1	E	328	PRO

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Mol	Chain	Res	Type
1	E	576	SER
1	C	399	THR
1	E	565	PRO
1	E	396	ILE
1	E	349	ILE

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	259/257 (101%)	234 (90%)	25 (10%)	8 31
1	C	259/257 (101%)	240 (93%)	19 (7%)	14 46
1	E	258/257 (100%)	230 (89%)	28 (11%)	6 26
2	B	150/156 (96%)	139 (93%)	11 (7%)	14 46
2	D	150/156 (96%)	142 (95%)	8 (5%)	22 58
2	F	150/156 (96%)	132 (88%)	18 (12%)	5 22
All	All	1226/1239 (99%)	1117 (91%)	109 (9%)	9 35

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	326	LEU
1	A	350	LEU
1	A	368	LEU
1	A	376	LEU
1	A	396	ILE
1	A	405	LEU
1	A	432	LEU
1	A	434	THR
1	A	438	ASN
1	A	443	SER
1	A	449	GLU
1	A	454	LEU
1	A	462	SER

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Mol	Chain	Res	Type
1	A	468	GLN
1	A	485	LYS
1	A	494	GLU
1	A	512	LEU
1	A	519	GLU
1	A	525	SER
1	A	526	PHE
1	A	572	GLU
1	A	594	LYS
1	A	597	THR
1	A	617	SER
1	A	619	LYS
2	B	37	THR
2	B	39	SER
2	B	52	THR
2	B	82	ARG
2	B	92	ASP
2	B	97	GLU
2	B	128	LEU
2	B	130	THR
2	B	137	THR
2	B	153	THR
2	B	168	MSE
1	C	326	LEU
1	C	330	THR
1	C	332	LEU
1	C	350	LEU
1	C	376	LEU
1	C	384	THR
1	C	397	ASP
1	C	432	LEU
1	C	443	SER
1	C	455	TYR
1	C	468	GLN
1	C	497	THR
1	C	518	LYS
1	C	522	LYS
1	C	526	PHE
1	C	565	PRO
1	C	572	GLU
1	C	578	LYS
1	C	579	LYS

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Mol	Chain	Res	Type
2	D	94	THR
2	D	104	GLN
2	D	120	LEU
2	D	128	LEU
2	D	135	ASP
2	D	137	THR
2	D	138	THR
2	D	168	MSE
1	E	344	ASN
1	E	363	ASN
1	E	366	ASN
1	E	376	LEU
1	E	379	ASP
1	E	385	CYS
1	E	396	ILE
1	E	401	ASN
1	E	403	PHE
1	E	432	LEU
1	E	438	ASN
1	E	443	SER
1	E	449	GLU
1	E	458	GLU
1	E	460	LYS
1	E	462	SER
1	E	479	ASN
1	E	485	LYS
1	E	497	THR
1	E	517	ILE
1	E	533	LYS
1	E	546	LEU
1	E	571	ILE
1	E	583	ARG
1	E	586	SER
1	E	588	PHE
1	E	604	ILE
1	E	616	ILE
2	F	11	LEU
2	F	26	CYS
2	F	34	ASP
2	F	49	LYS
2	F	53	ILE
2	F	66	ASP

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Mol	Chain	Res	Type
2	F	70	GLN
2	F	72	ARG
2	F	79	SER
2	F	85	HIS
2	F	91	TYR
2	F	102	VAL
2	F	110	ASP
2	F	121	LEU
2	F	124	ASN
2	F	146	LEU
2	F	166	MSE
2	F	167	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	HIS
2	B	63	GLN
1	C	366	ASN
2	D	85	HIS
2	D	118	ASN
2	D	157	ASN
2	D	160	ASN
1	E	441	ASN
1	E	475	ASN
1	E	532	ASN
1	E	553	GLN
2	F	70	GLN
2	F	118	ASN
2	F	124	ASN
2	F	163	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 35 ligands modelled in this entry, 9 are monoatomic - leaving 26 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	GOL	A	907	-	5,5,5	0.41	0	5,5,5	0.28	0
3	ACT	D	205	-	1,3,3	1.91	0	0,3,3	0.00	-
3	ACT	C	706	-	1,3,3	1.91	0	0,3,3	0.00	-
3	ACT	C	704	-	1,3,3	1.75	0	0,3,3	0.00	-
3	ACT	B	204	-	1,3,3	1.86	0	0,3,3	0.00	-
8	AF3	D	203	-	0,3,3	0.00	-	-	-	-
3	ACT	A	902	5	1,3,3	2.01	1 (100%)	0,3,3	0.00	-
4	GOL	C	707	-	5,5,5	0.49	0	5,5,5	0.17	0
7	GDP	B	202	6	24,30,30	1.34	3 (12%)	31,47,47	1.92	8 (25%)
3	ACT	B	205	-	1,3,3	1.74	0	0,3,3	0.00	-
7	GDP	F	201	6	24,30,30	1.34	2 (8%)	31,47,47	1.97	6 (19%)
3	ACT	A	901	-	1,3,3	2.37	1 (100%)	0,3,3	0.00	-
8	AF3	F	202	-	0,3,3	0.00	-	-	-	-
3	ACT	D	204	-	1,3,3	1.86	0	0,3,3	0.00	-
3	ACT	C	702	-	1,3,3	2.06	1 (100%)	0,3,3	0.00	-
4	GOL	A	903	-	5,5,5	0.50	0	5,5,5	0.83	0
4	GOL	A	908	-	5,5,5	0.31	0	5,5,5	0.30	0
8	AF3	B	203	-	0,3,3	0.00	-	-	-	-
4	GOL	A	904	-	5,5,5	0.36	0	5,5,5	0.43	0
3	ACT	C	703	-	1,3,3	2.31	1 (100%)	0,3,3	0.00	-
4	GOL	B	206	-	5,5,5	0.53	0	5,5,5	0.42	0
3	ACT	C	705	-	1,3,3	1.65	0	0,3,3	0.00	-
4	GOL	A	906	-	5,5,5	0.64	0	5,5,5	0.80	0
3	ACT	C	701	-	1,3,3	2.39	1 (100%)	0,3,3	0.00	-
4	GOL	A	905	-	5,5,5	0.48	0	5,5,5	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GDP	D	202	6	24,30,30	1.45	2 (8%)	31,47,47	1.87	7 (22%)

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	GOL	A	907	-	-	2/4/4/4	-
4	GOL	B	206	-	-	3/4/4/4	-
4	GOL	A	903	-	-	2/4/4/4	-
4	GOL	A	908	-	-	2/4/4/4	-
4	GOL	A	906	-	-	2/4/4/4	-
4	GOL	A	905	-	-	1/4/4/4	-
7	GDP	F	201	6	-	0/12/32/32	0/3/3/3
7	GDP	D	202	6	-	2/12/32/32	0/3/3/3
4	GOL	A	904	-	-	4/4/4/4	-
4	GOL	C	707	-	-	2/4/4/4	-
7	GDP	B	202	6	-	0/12/32/32	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	202	GDP	C6-C5	5.42	1.50	1.41
7	F	201	GDP	C6-C5	4.76	1.49	1.41
7	B	202	GDP	C6-C5	4.68	1.49	1.41
7	F	201	GDP	C5-C4	2.82	1.48	1.40
7	D	202	GDP	C5-C4	2.79	1.48	1.40
3	C	701	ACT	CH3-C	2.39	1.51	1.48
7	B	202	GDP	C5-C4	2.38	1.47	1.40
3	A	901	ACT	CH3-C	2.37	1.51	1.48
3	C	703	ACT	CH3-C	2.31	1.51	1.48
7	B	202	GDP	O4'-C1'	2.12	1.44	1.41
3	C	702	ACT	CH3-C	2.06	1.51	1.48
3	A	902	ACT	CH3-C	2.01	1.51	1.48

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	201	GDP	C2-N3-C4	5.73	121.90	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	202	GDP	C2-N3-C4	5.55	121.70	115.36
7	B	202	GDP	C2-N3-C4	5.50	121.64	115.36
7	B	202	GDP	C5-C6-N1	-4.34	117.50	123.43
7	D	202	GDP	C5-C6-N1	-4.05	117.89	123.43
7	F	201	GDP	C6-N1-C2	4.01	122.30	115.93
7	D	202	GDP	C4-C5-N7	-3.84	105.40	109.40
7	F	201	GDP	C5-C6-N1	-3.63	118.46	123.43
7	F	201	GDP	C6-C5-C4	-3.59	117.37	120.80
7	F	201	GDP	N3-C2-N1	-3.57	122.46	127.22
7	B	202	GDP	C4-C5-N7	-3.47	105.78	109.40
7	B	202	GDP	C6-N1-C2	3.41	121.34	115.93
7	D	202	GDP	C6-N1-C2	3.13	120.90	115.93
7	F	201	GDP	C4-C5-N7	-2.80	106.48	109.40
7	B	202	GDP	N3-C2-N1	-2.47	123.93	127.22
7	B	202	GDP	C3'-C2'-C1'	2.40	104.59	100.98
7	B	202	GDP	C6-C5-C4	-2.33	118.57	120.80
7	D	202	GDP	N3-C2-N1	-2.26	124.20	127.22
7	D	202	GDP	O3B-PB-O1B	2.13	119.03	110.68
7	D	202	GDP	C6-C5-C4	-2.11	118.79	120.80
7	B	202	GDP	O3B-PB-O1B	2.07	118.79	110.68

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	907	GOL	C1-C2-C3-O3
4	A	907	GOL	O2-C2-C3-O3
4	B	206	GOL	O1-C1-C2-C3
4	C	707	GOL	O2-C2-C3-O3
4	A	904	GOL	O2-C2-C3-O3
4	C	707	GOL	C1-C2-C3-O3
4	A	903	GOL	O1-C1-C2-C3
4	A	904	GOL	C1-C2-C3-O3
4	A	906	GOL	C1-C2-C3-O3
4	A	905	GOL	C1-C2-C3-O3
4	A	903	GOL	O1-C1-C2-O2
4	B	206	GOL	O1-C1-C2-O2
7	D	202	GDP	O4'-C4'-C5'-O5'
4	A	906	GOL	O2-C2-C3-O3
7	D	202	GDP	C3'-C4'-C5'-O5'
4	A	904	GOL	O1-C1-C2-O2
4	B	206	GOL	C1-C2-C3-O3

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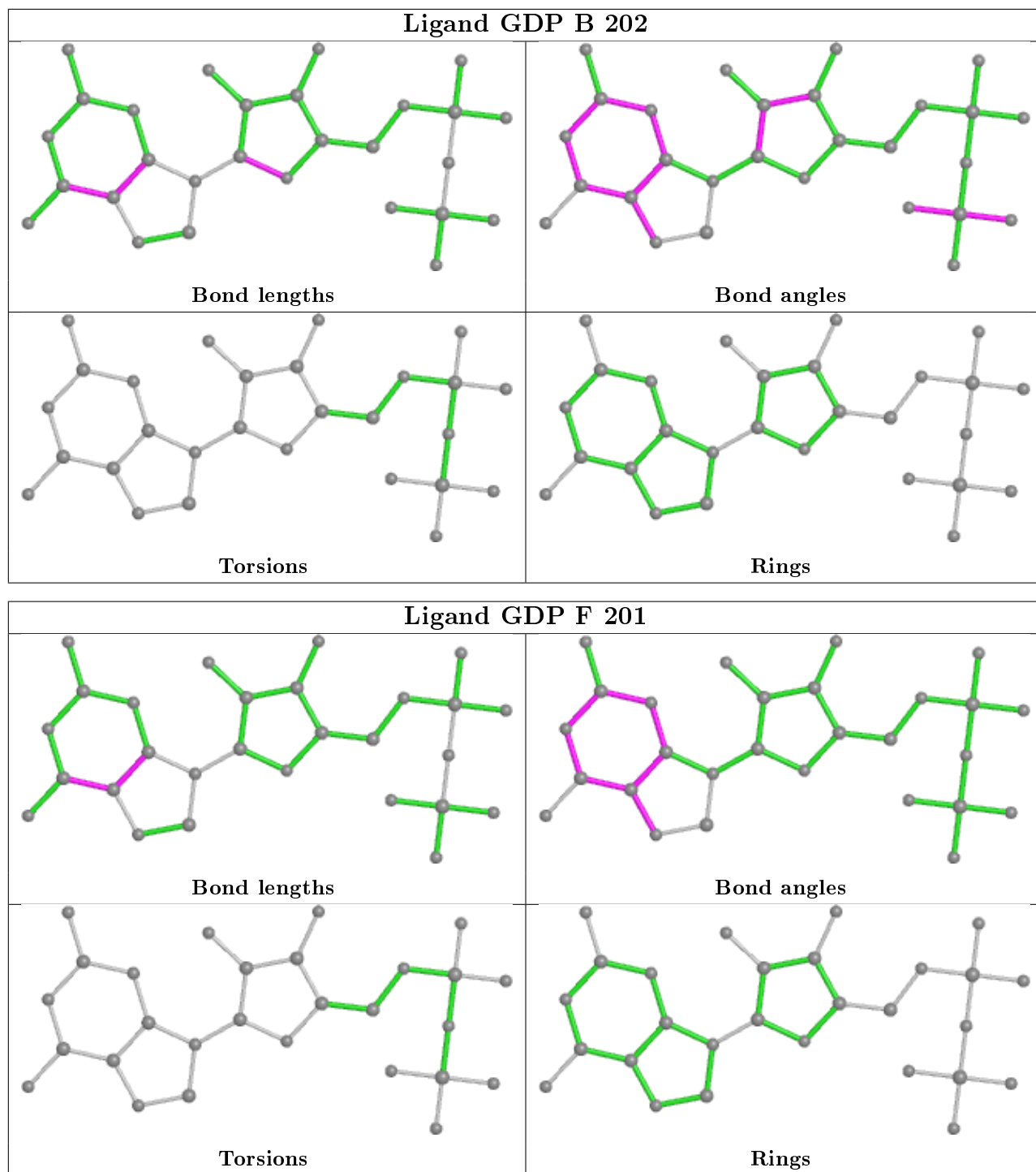
Mol	Chain	Res	Type	Atoms
4	A	908	GOL	O1-C1-C2-C3
4	A	908	GOL	O1-C1-C2-O2
4	A	904	GOL	O1-C1-C2-C3

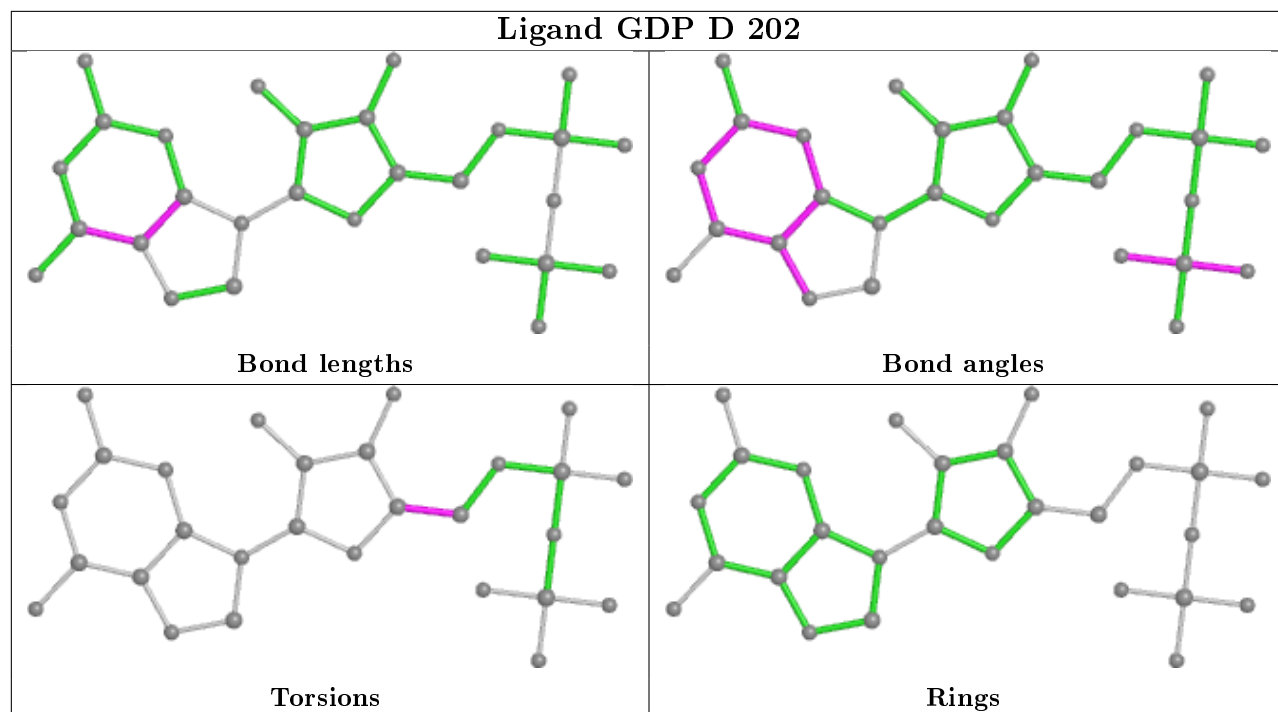
There are no ring outliers.

8 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	907	GOL	1	0
8	D	203	AF3	1	0
7	B	202	GDP	4	0
7	F	201	GDP	4	0
8	B	203	AF3	1	0
4	B	206	GOL	3	0
3	C	705	ACT	4	0
7	D	202	GDP	8	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

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, 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	293/299 (97%)	-0.42	3 (1%) 82 72	15, 36, 87, 158	0
1	C	293/299 (97%)	-0.44	2 (0%) 87 81	14, 36, 76, 112	0
1	E	292/299 (97%)	1.07	49 (16%) 1 1	55, 116, 178, 213	0
2	B	167/184 (90%)	-0.23	3 (1%) 68 55	17, 46, 96, 128	0
2	D	167/184 (90%)	-0.09	1 (0%) 89 83	22, 57, 100, 127	0
2	F	167/184 (90%)	2.09	69 (41%) 0 0	59, 133, 185, 213	0
All	All	1379/1449 (95%)	0.26	127 (9%) 9 5	14, 57, 162, 213	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	149	PRO	13.2
2	F	53	ILE	12.0
2	F	120	LEU	11.8
2	F	52	THR	8.0
2	F	148	ILE	7.9
2	F	96	GLN	7.6
2	F	150	PHE	7.6
1	E	554	LEU	7.5
1	E	531	PRO	6.8
2	F	165	PHE	6.8
1	E	452	CYS	6.4
2	F	163	GLN	6.1
1	E	530	LEU	5.9
2	F	170	ALA	5.9
2	F	121	LEU	5.5
1	E	568	SER	5.3
2	F	86	GLY	5.3
2	F	51	ARG	5.3
2	F	118	ASN	5.3

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Mol	Chain	Res	Type	RSRZ
1	E	325	SER	5.2
2	F	54	GLU	5.1
1	E	464	TRP	5.0
1	E	529	PRO	4.8
1	E	517	ILE	4.7
1	E	453	GLN	4.5
2	F	59	THR	4.4
2	F	164	SER	4.2
1	E	523	ALA	4.1
2	F	137	THR	4.1
2	F	68	ALA	4.0
1	E	592	VAL	4.0
1	E	565	PRO	3.9
2	F	130	THR	3.9
2	F	87	ILE	3.9
1	E	465	VAL	3.8
2	F	119	LYS	3.7
2	F	85	HIS	3.7
1	C	325	SER	3.7
2	D	57	GLY	3.6
1	E	515	ALA	3.6
1	A	530	LEU	3.6
2	F	133	VAL	3.6
2	F	8	TYR	3.6
2	F	60	ILE	3.6
2	F	10	TYR	3.5
2	F	147	GLY	3.4
1	E	356	GLU	3.4
1	E	467	ILE	3.4
2	F	129	THR	3.4
2	F	174	LYS	3.3
2	F	143	ALA	3.3
1	E	543	GLU	3.3
1	E	532	ASN	3.3
1	E	527	ALA	3.3
2	F	105	TRP	3.1
2	F	50	ILE	3.1
2	F	127	ASP	3.1
2	F	20	SER	3.0
1	E	528	GLU	3.0
1	E	469	THR	3.0
1	E	614	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	F	162	GLU	2.9
1	E	588	PHE	2.9
2	F	81	TYR	2.8
2	F	95	ASP	2.8
2	F	57	GLY	2.8
1	E	540	PRO	2.8
1	E	399	THR	2.8
1	E	397	ASP	2.8
1	E	416	GLY	2.7
2	F	115	GLU	2.7
2	F	94	THR	2.7
1	E	522	LYS	2.7
1	E	533	LYS	2.7
1	E	567	PRO	2.7
1	E	569	PRO	2.7
2	F	56	ASP	2.6
2	B	8	TYR	2.6
2	F	161	VAL	2.5
2	F	11	LEU	2.5
2	F	38	GLU	2.5
2	F	157	ASN	2.5
2	F	31	PHE	2.5
2	F	89	VAL	2.5
1	E	473	LEU	2.5
1	E	518	LYS	2.4
1	E	326	LEU	2.4
2	F	41	ILE	2.4
2	F	58	LYS	2.4
2	F	146	LEU	2.4
2	F	12	PHE	2.4
2	F	100	ASN	2.3
2	F	126	CYS	2.3
1	A	527	ALA	2.3
2	F	69	GLY	2.3
1	E	525	SER	2.3
1	E	492	ILE	2.3
1	E	458	GLU	2.3
2	F	152	GLU	2.3
1	E	443	SER	2.3
2	F	19	ASP	2.3
1	E	541	ILE	2.2
1	E	512	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
2	F	7	GLU	2.2
2	F	116	ASN	2.2
2	F	141	GLU	2.2
1	E	516	ASP	2.2
1	E	620	LYS	2.2
1	E	470	LEU	2.2
2	B	10	TYR	2.2
2	F	88	ILE	2.2
1	C	398	SER	2.1
1	E	521	LEU	2.1
2	F	128	LEU	2.1
1	E	358	PHE	2.1
2	F	144	ASP	2.1
1	A	528	GLU	2.1
1	E	474	GLY	2.1
1	E	524	PRO	2.1
2	F	43	THR	2.1
2	B	59(A)	THR	2.0
2	F	145	SER	2.0
2	F	151	LEU	2.0
2	F	39	SER	2.0
1	E	433	PHE	2.0
2	F	142	PHE	2.0
2	F	138	THR	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 carbohydrates in this entry.

6.4 Ligands [i](#)

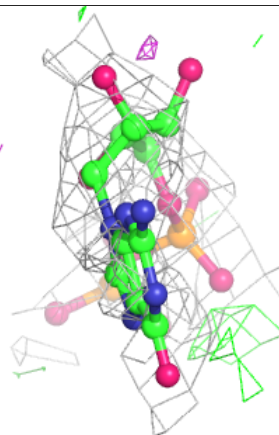
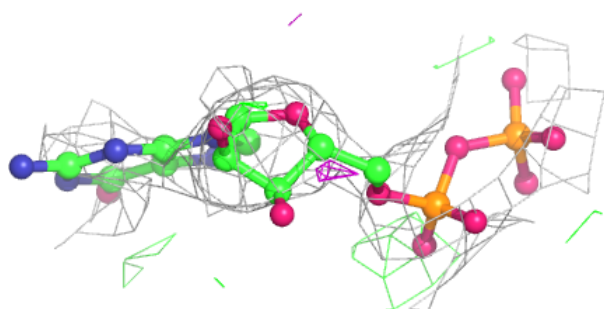
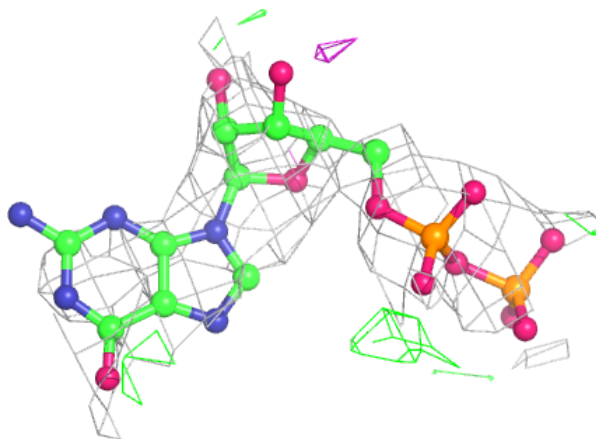
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	A	905	6/6	0.72	0.43	94,97,102,104	0
3	ACT	C	703	4/4	0.78	0.35	82,88,90,94	0
5	K	A	912	1/1	0.78	0.23	85,85,85,85	0
3	ACT	C	704	4/4	0.79	0.38	65,75,79,79	0
3	ACT	C	706	4/4	0.79	0.28	98,100,102,103	0
5	K	A	911	1/1	0.80	0.22	90,90,90,90	0
4	GOL	C	707	6/6	0.82	0.36	73,79,85,86	0
4	GOL	A	908	6/6	0.84	0.45	88,96,97,99	0
5	K	A	910	1/1	0.85	0.23	101,101,101,101	0
4	GOL	A	907	6/6	0.86	0.36	80,94,97,98	0
3	ACT	B	204	4/4	0.86	0.32	84,87,89,94	0
4	GOL	B	206	6/6	0.87	0.60	58,74,76,77	0
4	GOL	A	906	6/6	0.87	0.28	43,47,51,53	0
4	GOL	A	903	6/6	0.87	0.19	44,50,51,52	0
3	ACT	A	902	4/4	0.88	0.22	66,68,72,76	0
7	GDP	F	201	28/28	0.88	0.27	84,111,172,173	0
3	ACT	D	204	4/4	0.88	0.24	64,66,69,72	0
3	ACT	D	205	4/4	0.89	0.25	64,69,71,73	0
5	K	A	909	1/1	0.89	0.15	85,85,85,85	0
3	ACT	B	205	4/4	0.89	0.28	63,66,68,75	0
8	AF3	F	202	4/4	0.90	0.28	56,60,61,66	0
6	MG	B	201	1/1	0.90	0.18	32,32,32,32	0
3	ACT	C	701	4/4	0.90	0.39	59,61,65,67	0
4	GOL	A	904	6/6	0.90	0.44	61,68,73,78	0
3	ACT	C	702	4/4	0.90	0.30	60,63,65,65	0
3	ACT	A	901	4/4	0.91	0.20	51,54,56,57	0
3	ACT	C	705	4/4	0.91	0.74	88,88,94,100	0
5	K	B	207	1/1	0.96	0.13	52,52,52,52	0
5	K	C	708	1/1	0.96	0.14	72,72,72,72	0
8	AF3	B	203	4/4	0.97	0.24	31,32,33,33	0
6	MG	D	201	1/1	0.97	0.16	36,36,36,36	0
7	GDP	B	202	28/28	0.97	0.20	19,32,43,47	0
7	GDP	D	202	28/28	0.97	0.17	22,29,38,41	0
6	MG	F	200	1/1	0.98	0.10	45,45,45,45	0
8	AF3	D	203	4/4	0.98	0.18	29,30,30,30	0

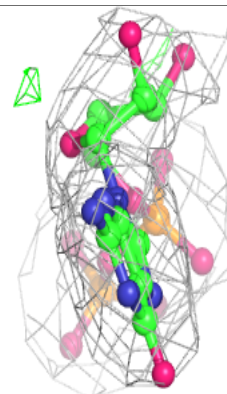
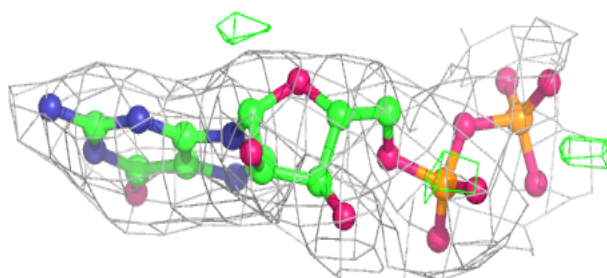
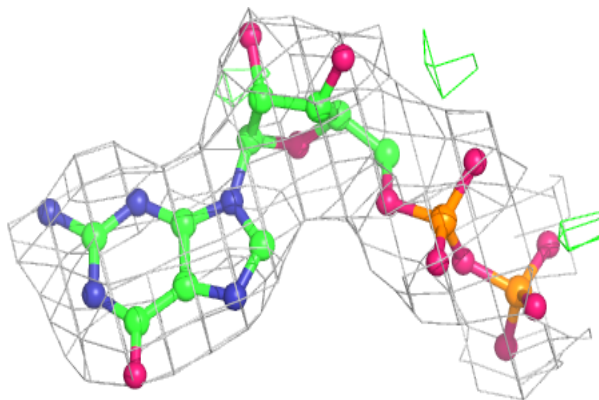
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

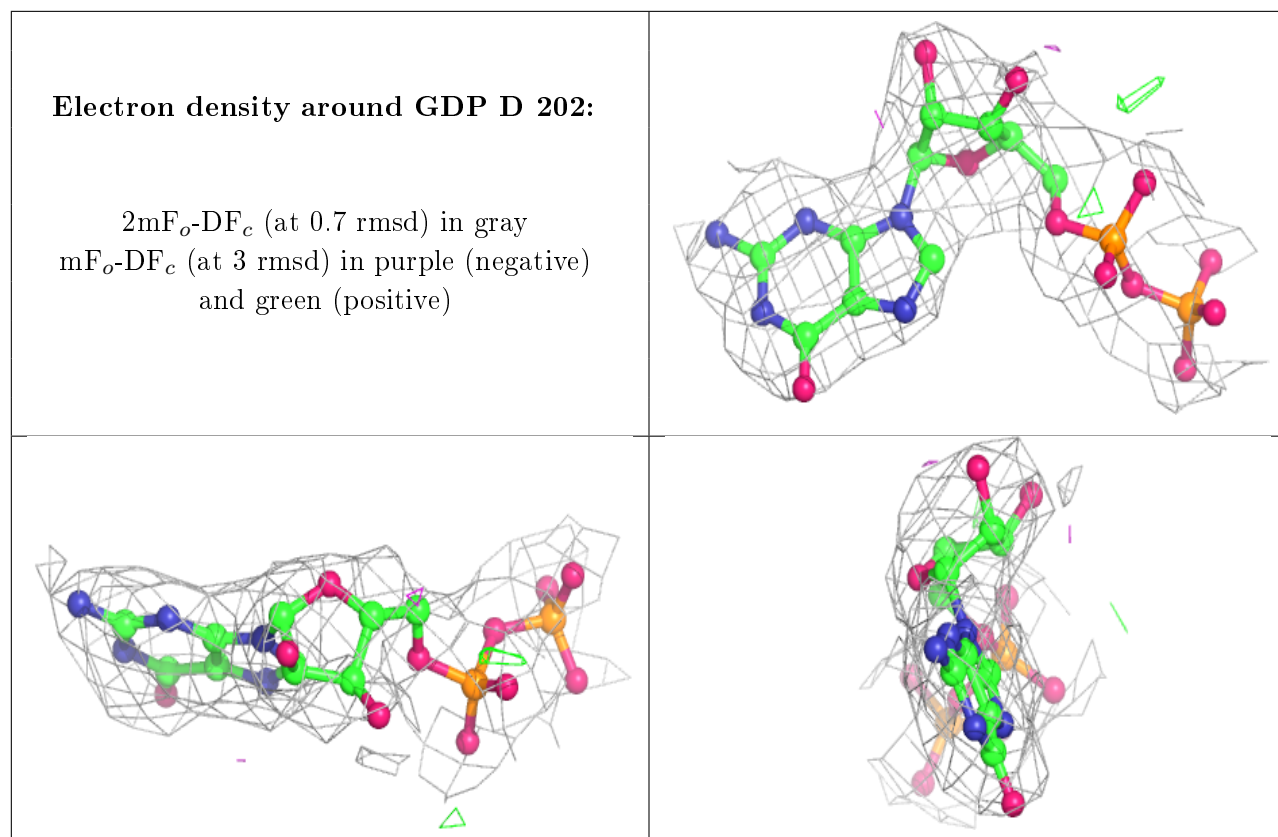
Electron density around GDP F 201:

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

**Electron density around GDP B 202:**

$2mF_o-DF_c$ (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.