



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 05:05 pm BST

PDB ID : 5JCZ
Title : Rab11 bound to MyoVa-GTD
Authors : Pylypenko, O.; Attanda, W.; Gauquelin, C.; Malherbes, G.; Houdusse, A.
Deposited on : 2016-04-15
Resolution : 2.06 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

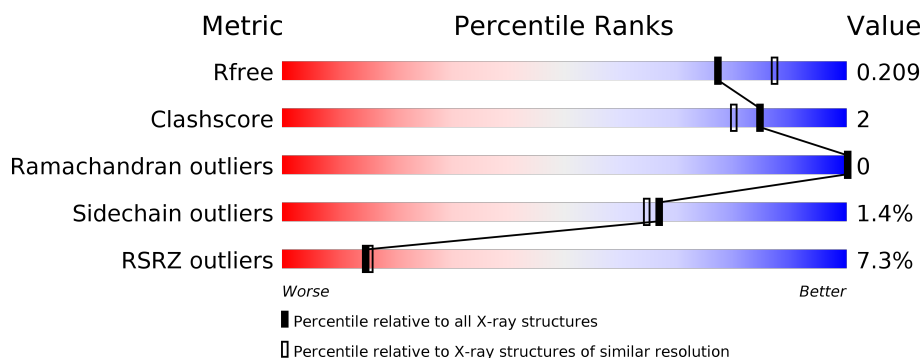
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	179	<div> <div>90%</div> <div>6% •</div> </div>
1	D	179	<div> <div>%</div> <div>92%</div> <div>• • •</div> </div>
1	I	179	<div> <div>46%</div> <div>81%</div> <div>• 18%</div> </div>
2	B	397	<div> <div>4%</div> <div>85%</div> <div>6% • 8%</div> </div>
2	C	397	<div> <div>%</div> <div>85%</div> <div>7% 8%</div> </div>
2	E	397	<div> <div>3%</div> <div>83%</div> <div>7% • 9%</div> </div>

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 13842 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 Ras-related protein Rab-11A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	6	0
			1391	883	236	271	1			
1	D	173	Total	C	N	O	S	0	3	0
			1386	880	239	266	1			
1	I	147	Total	C	N	O	S	0	0	0
			980	606	176	197	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P62491
A	0	ALA	-	expression tag	UNP P62491
D	-1	GLY	-	expression tag	UNP P62491
D	0	ALA	-	expression tag	UNP P62491
I	-1	GLY	-	expression tag	UNP P62491
I	0	ALA	-	expression tag	UNP P62491

- Molecule 2 is a protein called Unconventional myosin-Va.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	364	Total	C	N	O	S	0	3	0
			2891	1852	490	526	23			
2	C	364	Total	C	N	O	S	0	8	0
			2948	1882	501	541	24			
2	E	361	Total	C	N	O	S	0	6	0
			2920	1861	500	537	22			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1457	GLY	-	expression tag	UNP Q9Y4I1
B	1458	ALA	-	expression tag	UNP Q9Y4I1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1459	MET	-	expression tag	UNP Q9Y4I1
B	1460	GLY	-	expression tag	UNP Q9Y4I1
B	1461	SER	-	expression tag	UNP Q9Y4I1
C	1457	GLY	-	expression tag	UNP Q9Y4I1
C	1458	ALA	-	expression tag	UNP Q9Y4I1
C	1459	MET	-	expression tag	UNP Q9Y4I1
C	1460	GLY	-	expression tag	UNP Q9Y4I1
C	1461	SER	-	expression tag	UNP Q9Y4I1
E	1457	GLY	-	expression tag	UNP Q9Y4I1
E	1458	ALA	-	expression tag	UNP Q9Y4I1
E	1459	MET	-	expression tag	UNP Q9Y4I1
E	1460	GLY	-	expression tag	UNP Q9Y4I1
E	1461	SER	-	expression tag	UNP Q9Y4I1

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

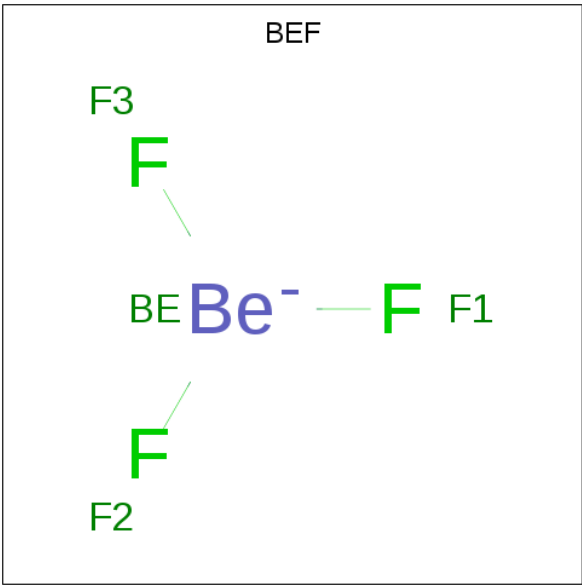
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	I	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
4	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
4	I	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 5 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula: BeF₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Be	F	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total 4	Be 1	F 3	0	0
5	I	1	Total 4	Be 1	F 3	0	0

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



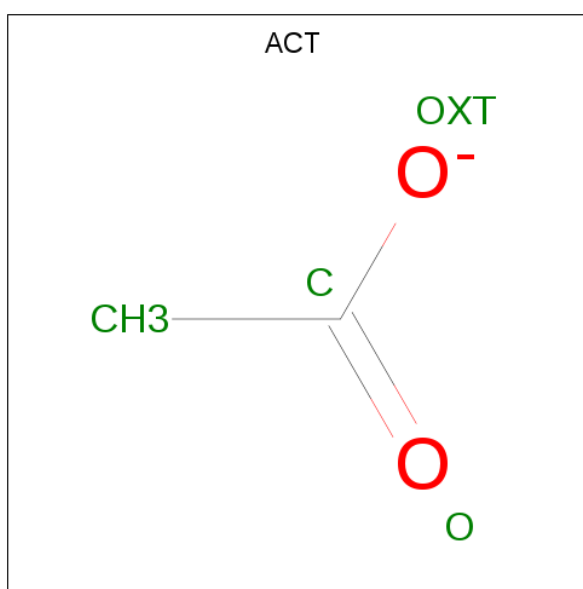
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		
6	E	1	Total	C	O	0	0
			4	2	2		
6	E	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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


- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	210	Total	O	0	0
			210	210		
9	B	163	Total	O	0	0
			163	163		
9	C	377	Total	O	0	0
			377	377		
9	D	146	Total	O	0	0
			146	146		
9	E	250	Total	O	0	0
			250	250		
9	I	8	Total	O	0	0
			8	8		

3 Residue-property plots [i](#)

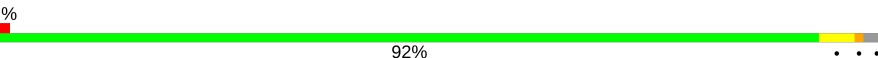
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

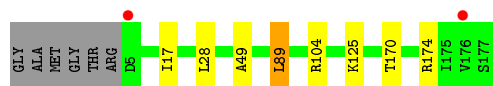
- Molecule 1: Ras-related protein Rab-11A

Chain A: 




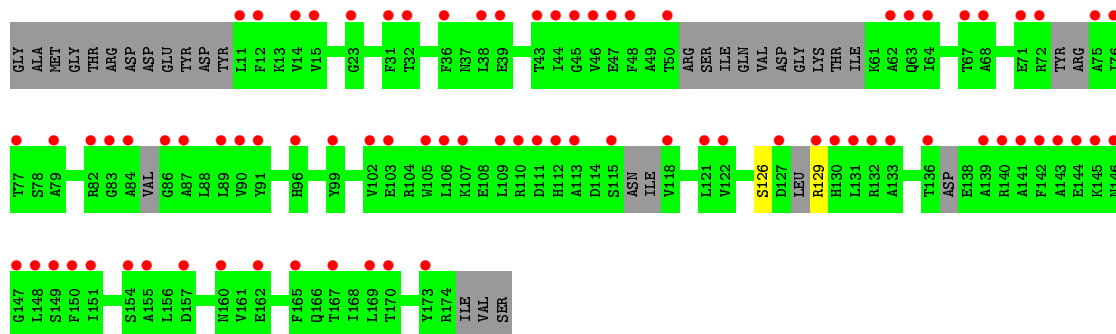
- Molecule 1: Ras-related protein Rab-11A

Chain D: 




- Molecule 1: Ras-related protein Rab-11A

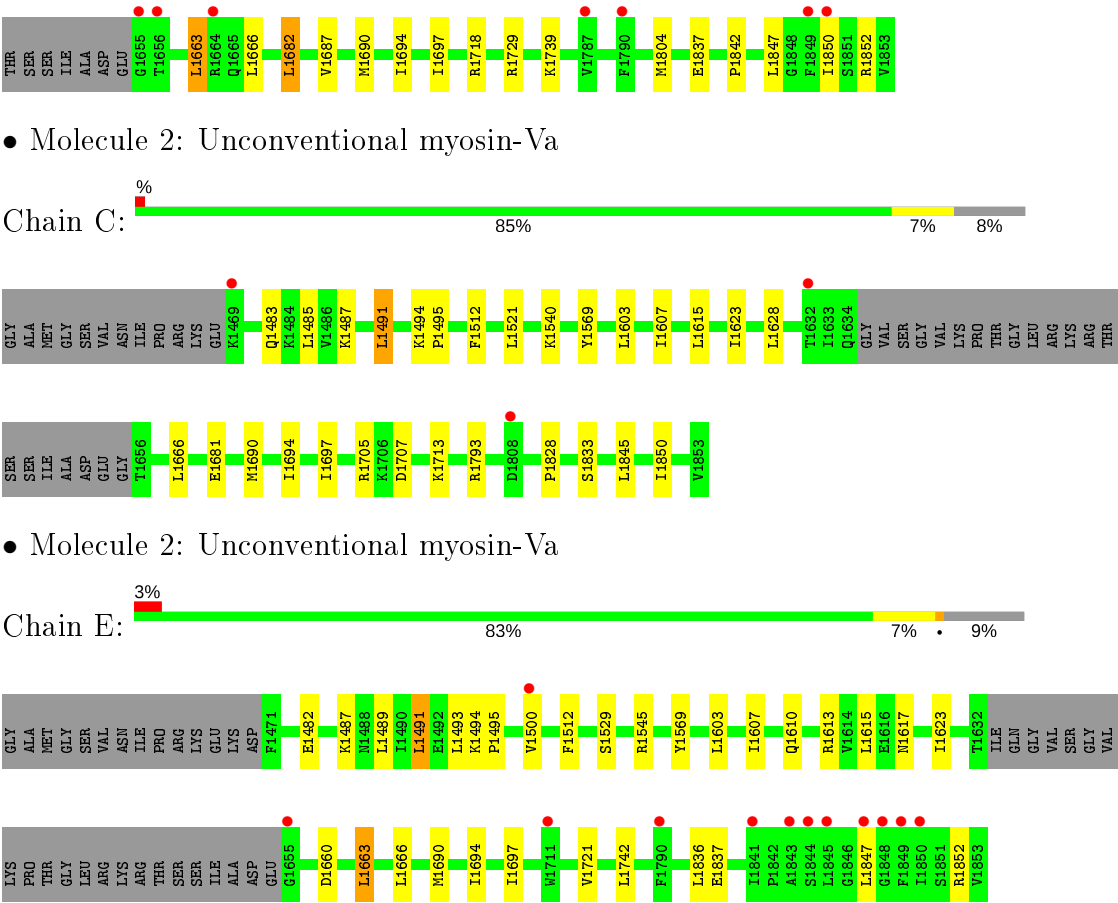
Chain I: 



- Molecule 2: Unconventional myosin-Va

Chain B: 





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	215.79Å 128.42Å 89.02Å 90.00° 98.27° 90.00°	Depositor
Resolution (Å)	48.88 – 2.06 48.88 – 2.06	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.88-2.06) 98.6 (48.88-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.180 , 0.208 0.181 , 0.209	Depositor DCC
R_{free} test set	7339 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 61.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13842	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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, BEF, EDO, ACT

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	0.21	0/1431	0.40	0/1934
1	D	0.21	0/1411	0.39	0/1908
1	I	0.21	0/986	0.38	0/1339
2	B	0.21	0/2949	0.37	0/3982
2	C	0.21	0/3021	0.37	0/4077
2	E	0.21	0/2988	0.37	0/4034
All	All	0.21	0/12786	0.38	0/17274

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1391	0	1388	8	0
1	D	1386	0	1375	4	0
1	I	980	0	804	1	0
2	B	2891	0	2917	16	0
2	C	2948	0	3012	16	0
2	E	2920	0	2965	16	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	I	1	0	0	0	0
4	A	28	0	12	1	0
4	D	28	0	12	1	0
4	I	28	0	12	0	0
5	A	4	0	0	0	0
5	D	4	0	0	0	0
5	I	4	0	0	0	0
6	A	12	0	18	2	0
6	B	8	0	12	0	0
6	C	16	0	24	2	0
6	D	8	0	12	0	0
6	E	8	0	12	0	0
7	A	4	0	3	0	0
7	C	4	0	3	0	0
8	A	6	0	8	0	0
8	B	6	0	8	2	0
9	A	210	0	0	0	0
9	B	163	0	0	0	0
9	C	377	0	0	2	0
9	D	146	0	0	0	0
9	E	250	0	0	1	0
9	I	8	0	0	0	0
All	All	13842	0	12597	59	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 2.

All (59) 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:28[B]:LEU:HD11	1:A:49:ALA:HB3	1.68	0.74
2:C:1623:ILE:HD12	2:C:1697:ILE:HD12	1.70	0.73
2:C:1491:LEU:HG	6:C:1903:EDO:H12	1.70	0.72
2:B:1623[A]:ILE:HD12	2:B:1697:ILE:HD12	1.73	0.71
1:D:28[B]:LEU:HD11	1:D:49:ALA:HB3	1.71	0.71
2:C:1623:ILE:HD13	2:C:1694:ILE:HA	1.76	0.66
2:B:1623[A]:ILE:HD13	2:B:1694:ILE:HA	1.80	0.63
2:E:1623:ILE:HD12	2:E:1697:ILE:HD12	1.83	0.60
2:C:1615:LEU:HD13	2:C:1690:MET:HG2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1487:LYS:HA	2:C:1491:LEU:HB2	1.85	0.57
2:E:1623:ILE:HD13	2:E:1694:ILE:HA	1.86	0.57
2:E:1615:LEU:HD13	2:E:1690:MET:HG2	1.86	0.56
2:E:1617[B]:ASN:ND2	9:E:2004:HOH:O	2.33	0.55
2:E:1491:LEU:O	2:E:1545:ARG:NH1	2.41	0.54
2:C:1540:LYS:HE2	6:C:1903:EDO:H11	1.90	0.53
2:B:1837:GLU:O	2:B:1852:ARG:NH1	2.41	0.53
2:E:1610[A]:GLN:OE1	2:E:1613:ARG:NH1	2.33	0.51
2:E:1603:LEU:O	2:E:1607:ILE:HG13	2.12	0.50
2:E:1837:GLU:O	2:E:1852:ARG:NH1	2.42	0.49
2:E:1487:LYS:HA	2:E:1491:LEU:HB2	1.94	0.49
1:A:17:ILE:HG22	6:A:204:EDO:H21	1.94	0.48
1:D:125:LYS:HG2	4:D:202:GDP:C6	2.48	0.48
2:C:1793:ARG:NH1	9:C:2015:HOH:O	2.46	0.48
2:E:1721:VAL:HG13	2:E:1742:LEU:HD23	1.96	0.48
1:A:125:LYS:HG2	4:A:202:GDP:C6	2.49	0.47
1:A:129:ARG:HB3	6:A:205:EDO:H12	1.97	0.47
2:B:1499:ALA:HB1	2:B:1842:PRO:HG2	1.96	0.47
2:C:1628:LEU:O	2:C:1713:LYS:NZ	2.36	0.47
2:C:1603:LEU:O	2:C:1607:ILE:HG13	2.15	0.46
2:B:1603:LEU:O	2:B:1607:ILE:HG13	2.14	0.46
2:C:1485:LEU:HG	2:C:1850:ILE:HD11	1.97	0.45
2:C:1512:PHE:CZ	2:C:1569:TYR:HB2	2.51	0.45
2:B:1512:PHE:CZ	2:B:1569:TYR:HB2	2.51	0.45
2:E:1489:LEU:HD13	2:E:1847:LEU:HD11	1.99	0.45
1:A:33:ARG:HD2	2:B:1729:ARG:NH2	2.33	0.44
2:C:1705:ARG:HB3	2:C:1707:ASP:OD1	2.18	0.44
2:E:1512:PHE:CZ	2:E:1569:TYR:HB2	2.53	0.44
2:C:1483:GLN:NE2	9:C:2008:HOH:O	2.36	0.43
2:E:1493:LEU:HD21	2:E:1500:VAL:HG21	2.00	0.43
1:A:94:ALA:O	2:C:1833[B]:SER:OG	2.35	0.43
2:B:1491:LEU:HD11	2:B:1540:LYS:HD3	2.01	0.42
2:B:1682:LEU:HA	2:B:1682:LEU:HD12	1.91	0.42
1:D:17:ILE:HD11	1:D:89:LEU:HG	2.02	0.42
1:A:12:PHE:CE1	1:A:60:ILE:HD13	2.55	0.41
1:D:170:THR:O	1:D:174:ARG:HG2	2.19	0.41
2:E:1482:GLU:OE2	2:E:1529:SER:OG	2.24	0.41
2:B:1663:LEU:HA	2:B:1663:LEU:HD12	1.83	0.41
1:A:145:LYS:HB2	1:A:145:LYS:HE3	1.83	0.41
2:B:1485:LEU:HD13	2:B:1850:ILE:HD11	2.01	0.41
2:C:1494:LYS:HA	2:C:1495:PRO:HD3	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1494:LYS:HA	2:E:1495:PRO:HD3	1.88	0.41
2:B:1718:ARG:HA	2:B:1718:ARG:HD2	1.89	0.40
2:B:1847:LEU:HB3	2:B:1850:ILE:HD12	2.03	0.40
2:E:1663:LEU:HD12	2:E:1663:LEU:HA	1.89	0.40
1:I:126:SER:O	1:I:129:ARG:HB2	2.21	0.40
2:B:1687:VAL:HA	2:B:1690:MET:HE2	2.02	0.40
2:C:1681:GLU:HB2	2:C:1828:PRO:HG3	2.02	0.40
2:B:1718:ARG:NH2	8:B:1903:GOL:H11	2.36	0.40
2:B:1739:LYS:HZ1	8:B:1903:GOL:H12	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	176/179 (98%)	175 (99%)	1 (1%)	0	100	100
1	D	174/179 (97%)	173 (99%)	1 (1%)	0	100	100
1	I	133/179 (74%)	130 (98%)	3 (2%)	0	100	100
2	B	363/397 (91%)	353 (97%)	10 (3%)	0	100	100
2	C	368/397 (93%)	359 (98%)	9 (2%)	0	100	100
2	E	363/397 (91%)	359 (99%)	4 (1%)	0	100	100
All	All	1577/1728 (91%)	1549 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	150/150 (100%)	149 (99%)	1 (1%)	84	84
1	D	146/150 (97%)	144 (99%)	2 (1%)	67	64
1	I	77/150 (51%)	77 (100%)	0	100	100
2	B	316/360 (88%)	310 (98%)	6 (2%)	57	53
2	C	335/360 (93%)	331 (99%)	4 (1%)	71	69
2	E	328/360 (91%)	323 (98%)	5 (2%)	65	62
All	All	1352/1530 (88%)	1334 (99%)	18 (1%)	67	67

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	ARG
2	B	1471	PHE
2	B	1609	GLN
2	B	1663	LEU
2	B	1666	LEU
2	B	1682	LEU
2	B	1804	MET
2	C	1491	LEU
2	C	1521	LEU
2	C	1666	LEU
2	C	1845	LEU
1	D	89	LEU
1	D	104	ARG
2	E	1491	LEU
2	E	1660	ASP
2	E	1663	LEU
2	E	1666	LEU
2	E	1836	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	1586	HIS
2	C	1609	GLN
2	E	1517	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 27 ligands modelled in this entry, 4 are monoatomic - leaving 23 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	$\# Z > 2$
8	GOL	B	1903	-	5,5,5	0.36	0	5,5,5	0.35	0
7	ACT	A	207	-	1,3,3	1.36	0	0,3,3	0.00	-
6	EDO	E	1901	-	3,3,3	0.47	0	2,2,2	0.28	0
6	EDO	C	1903	-	3,3,3	0.45	0	2,2,2	0.33	0
6	EDO	E	1902	-	3,3,3	0.46	0	2,2,2	0.27	0
8	GOL	A	208	-	5,5,5	0.33	0	5,5,5	0.31	0
6	EDO	C	1902	-	3,3,3	0.46	0	2,2,2	0.30	0
6	EDO	A	205	-	3,3,3	0.45	0	2,2,2	0.34	0
6	EDO	C	1901	-	3,3,3	0.47	0	2,2,2	0.31	0
6	EDO	A	206	-	3,3,3	0.45	0	2,2,2	0.33	0
6	EDO	C	1904	-	3,3,3	0.45	0	2,2,2	0.36	0
6	EDO	B	1901	-	3,3,3	0.47	0	2,2,2	0.30	0
6	EDO	D	205	-	3,3,3	0.46	0	2,2,2	0.30	0
7	ACT	C	1906	-	1,3,3	1.31	0	0,3,3	0.00	-
5	BEF	I	203	4	0,3,3	0.00	-	-	-	-
6	EDO	B	1902	-	3,3,3	0.46	0	2,2,2	0.32	0
4	GDP	A	202	3,5	24,30,30	1.16	2 (8%)	31,47,47	1.90	7 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	A	204	-	3,3,3	0.47	0	2,2,2	0.30	0
4	GDP	D	202	3,5	24,30,30	1.20	2 (8%)	31,47,47	1.97	7 (22%)
6	EDO	D	204	-	3,3,3	0.45	0	2,2,2	0.32	0
5	BEF	A	203	4	0,3,3	0.00	-	-	-	-
4	GDP	I	202	3,5	24,30,30	1.18	2 (8%)	31,47,47	2.00	8 (25%)
5	BEF	D	203	4	0,3,3	0.00	-	-	-	-

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
8	GOL	A	208	-	-	2/4/4/4	-
6	EDO	B	1901	-	-	0/1/1/1	-
8	GOL	B	1903	-	-	2/4/4/4	-
6	EDO	C	1903	-	-	0/1/1/1	-
4	GDP	I	202	3,5	-	1/12/32/32	0/3/3/3
4	GDP	A	202	3,5	-	1/12/32/32	0/3/3/3
6	EDO	D	205	-	-	0/1/1/1	-
6	EDO	B	1902	-	-	0/1/1/1	-
6	EDO	D	204	-	-	0/1/1/1	-
6	EDO	A	204	-	-	0/1/1/1	-
6	EDO	C	1902	-	-	0/1/1/1	-
6	EDO	A	205	-	-	0/1/1/1	-
4	GDP	D	202	3,5	-	4/12/32/32	0/3/3/3
6	EDO	C	1901	-	-	0/1/1/1	-
6	EDO	E	1901	-	-	0/1/1/1	-
6	EDO	E	1902	-	-	0/1/1/1	-
6	EDO	A	206	-	-	0/1/1/1	-
6	EDO	C	1904	-	-	0/1/1/1	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	202	GDP	C6-C5	4.21	1.48	1.41
4	D	202	GDP	C6-C5	4.21	1.48	1.41
4	A	202	GDP	C6-C5	4.13	1.48	1.41
4	D	202	GDP	C5-C4	2.48	1.47	1.40
4	I	202	GDP	C5-C4	2.44	1.47	1.40
4	A	202	GDP	C5-C4	2.40	1.47	1.40

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	202	GDP	C2-N3-C4	4.85	120.89	115.36
4	D	202	GDP	C2-N3-C4	4.80	120.84	115.36
4	A	202	GDP	C2-N3-C4	4.59	120.60	115.36
4	A	202	GDP	C6-N1-C2	4.18	122.57	115.93
4	D	202	GDP	C6-N1-C2	4.15	122.53	115.93
4	D	202	GDP	C6-C5-C4	-4.12	116.86	120.80
4	I	202	GDP	C6-N1-C2	4.09	122.43	115.93
4	A	202	GDP	C5-C6-N1	-4.07	117.86	123.43
4	I	202	GDP	C5-C6-N1	-4.02	117.93	123.43
4	D	202	GDP	C5-C6-N1	-4.00	117.96	123.43
4	A	202	GDP	C6-C5-C4	-3.94	117.04	120.80
4	I	202	GDP	C6-C5-C4	-3.83	117.14	120.80
4	I	202	GDP	PA-O3A-PB	-3.59	120.50	132.83
4	D	202	GDP	N3-C2-N1	-3.39	122.71	127.22
4	A	202	GDP	N3-C2-N1	-3.33	122.78	127.22
4	I	202	GDP	N3-C2-N1	-3.32	122.80	127.22
4	D	202	GDP	PA-O3A-PB	-3.31	121.45	132.83
4	A	202	GDP	PA-O3A-PB	-3.03	122.44	132.83
4	I	202	GDP	C3'-C2'-C1'	2.97	105.45	100.98
4	D	202	GDP	C4-C5-N7	-2.74	106.54	109.40
4	I	202	GDP	C4-C5-N7	-2.70	106.58	109.40
4	A	202	GDP	C4-C5-N7	-2.66	106.63	109.40

There are no chirality outliers.

All (10) torsion outliers are listed below:

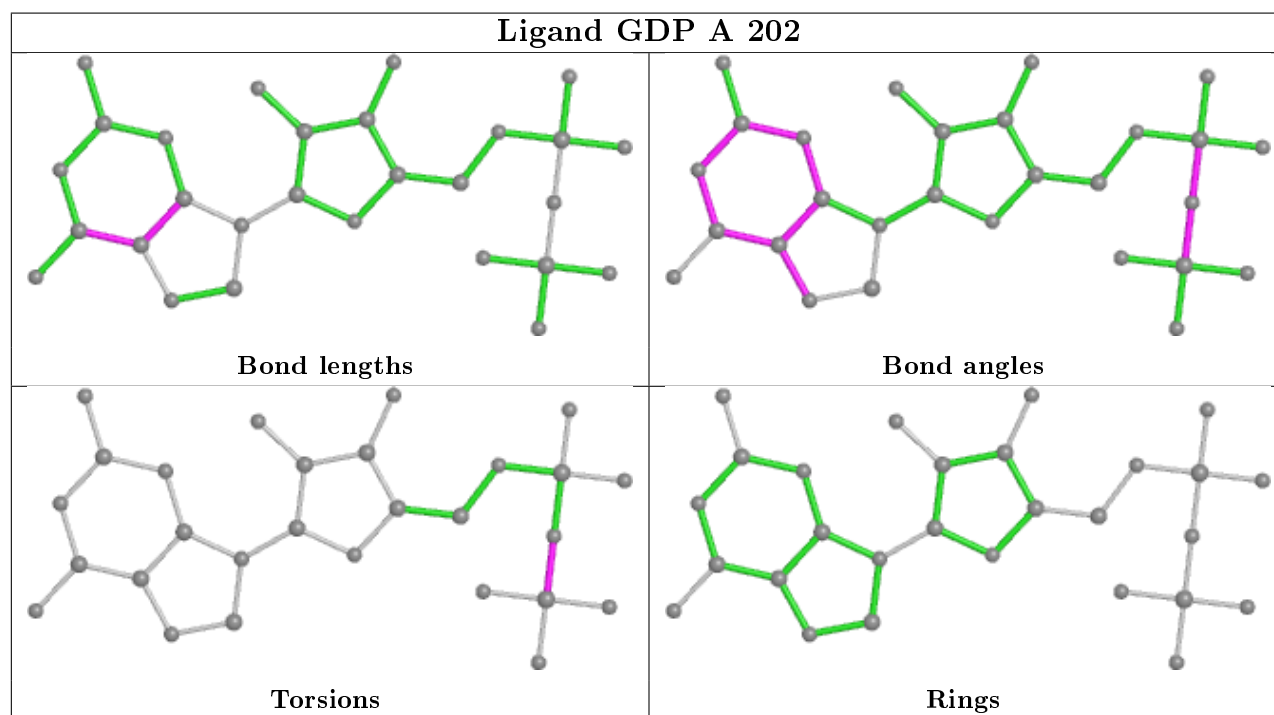
Mol	Chain	Res	Type	Atoms
4	A	202	GDP	PA-O3A-PB-O2B
4	D	202	GDP	PA-O3A-PB-O2B
4	D	202	GDP	PA-O3A-PB-O3B
4	I	202	GDP	PA-O3A-PB-O2B
8	B	1903	GOL	O1-C1-C2-C3
8	A	208	GOL	O1-C1-C2-C3
8	B	1903	GOL	O1-C1-C2-O2
8	A	208	GOL	O1-C1-C2-O2
4	D	202	GDP	PA-O3A-PB-O1B
4	D	202	GDP	C5'-O5'-PA-O1A

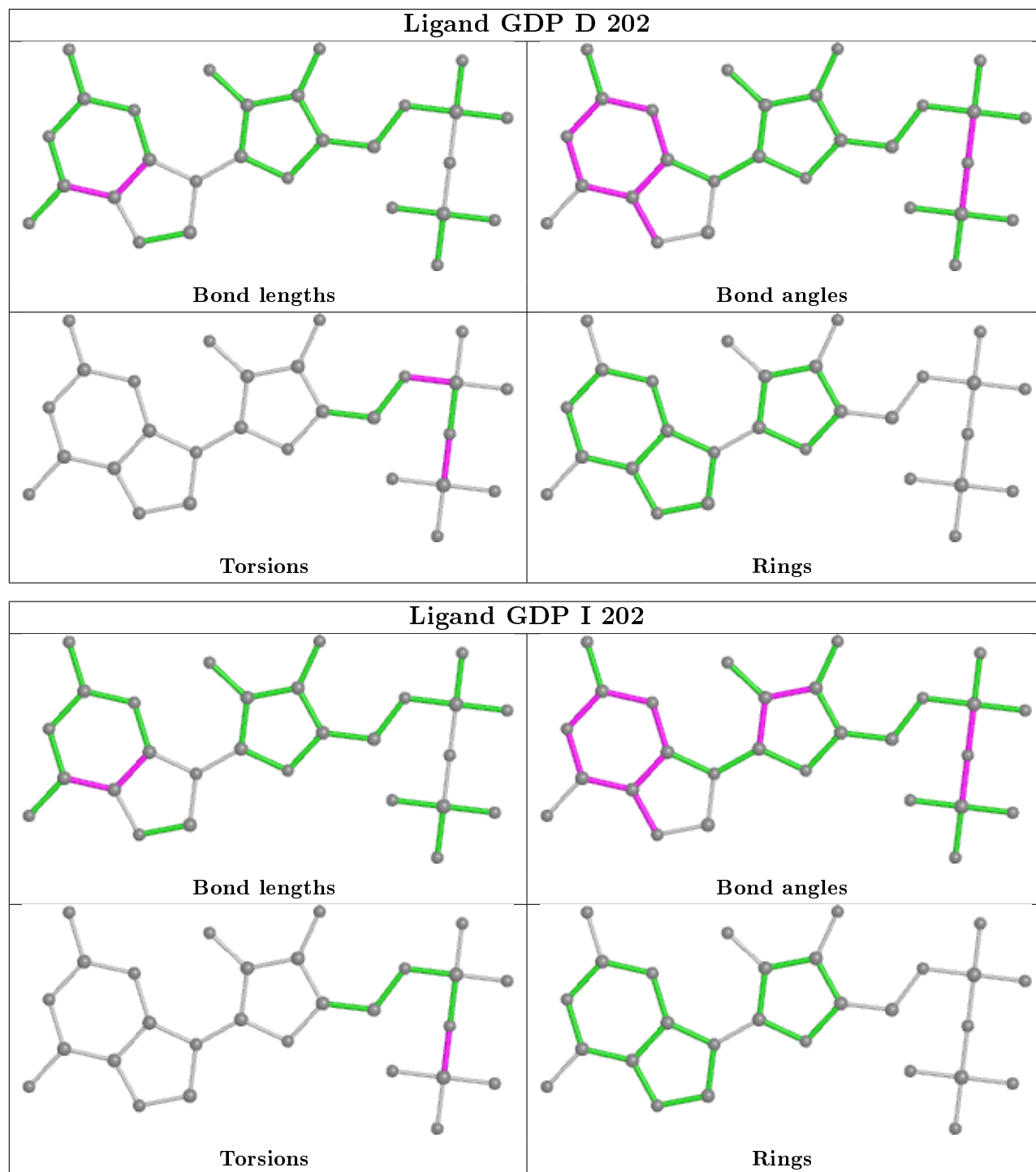
There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	1903	GOL	2	0
6	C	1903	EDO	2	0
6	A	205	EDO	1	0
4	A	202	GDP	1	0
6	A	204	EDO	1	0
4	D	202	GDP	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	172/179 (96%)	-0.03	0 100 100	35, 45, 66, 107	0
1	D	173/179 (96%)	-0.05	2 (1%) 79 80	41, 56, 84, 125	0
1	I	147/179 (82%)	2.67	82 (55%) 0 0	41, 51, 62, 72	147 (100%)
2	B	364/397 (91%)	0.21	16 (4%) 34 35	42, 72, 110, 131	0
2	C	364/397 (91%)	-0.06	3 (0%) 86 87	36, 49, 74, 120	1 (0%)
2	E	361/397 (90%)	0.17	12 (3%) 46 49	38, 57, 98, 120	1 (0%)
All	All	1581/1728 (91%)	0.31	115 (7%) 15 15	35, 55, 98, 131	149 (9%)

All (115) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	31	PHE	9.0
1	I	148	LEU	8.7
1	I	44	ILE	8.4
1	I	142	PHE	6.3
1	I	79	ALA	6.1
1	I	115	SER	6.0
1	I	121	LEU	6.0
1	I	76	ILE	6.0
1	I	102	VAL	5.9
1	I	122	VAL	5.7
1	I	169	LEU	5.7
1	I	106	LEU	5.6
1	I	165	PHE	5.6
1	I	149	SER	5.5
1	I	67	THR	5.4
1	I	91	TYR	5.4
2	E	1790	PHE	5.2
1	I	110	ARG	5.2
1	I	105	TRP	5.1

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Mol	Chain	Res	Type	RSRZ
2	B	1790	PHE	5.1
1	I	150	PHE	5.0
1	I	131	LEU	5.0
1	I	15	VAL	4.9
1	I	14	VAL	4.7
1	I	147	GLY	4.6
1	I	111	ASP	4.5
2	B	1655	GLY	4.5
1	I	46	VAL	4.4
1	I	89	LEU	4.3
1	I	143	ALA	4.2
2	E	1845	LEU	4.2
1	I	118	VAL	4.2
1	I	99	TYR	4.1
2	B	1656	THR	4.1
1	I	90	VAL	4.0
1	I	96	HIS	4.0
1	I	146	ASN	4.0
1	I	87	ALA	4.0
1	I	45	GLY	4.0
2	E	1850	ILE	4.0
1	D	5	ASP	3.9
1	I	12	PHE	3.8
1	I	160	ASN	3.8
2	E	1848	GLY	3.8
1	I	145	LYS	3.7
2	E	1849	PHE	3.7
1	D	176	VAL	3.6
1	I	83	GLY	3.6
2	E	1847	LEU	3.6
2	B	1787	VAL	3.6
1	I	86	GLY	3.6
2	B	1850	ILE	3.5
1	I	75	ALA	3.5
1	I	144	GLU	3.5
2	E	1655	GLY	3.5
1	I	11	LEU	3.4
2	E	1843	ALA	3.4
1	I	84	ALA	3.4
2	C	1469	LYS	3.3
1	I	155	ALA	3.3
1	I	130	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
1	I	62	ALA	3.3
1	I	103	GLU	3.2
1	I	173	TYR	3.2
1	I	141	ALA	3.2
2	B	1491	LEU	3.2
1	I	72	ARG	3.1
1	I	23	GLY	3.1
1	I	71	GLU	3.1
1	I	157	ASP	3.1
1	I	113	ALA	3.1
1	I	38	LEU	3.0
1	I	139	ALA	3.0
1	I	82	ARG	2.9
1	I	64	ILE	2.9
1	I	162	GLU	2.8
1	I	170	THR	2.8
1	I	77	THR	2.8
2	E	1844	SER	2.7
2	B	1493	LEU	2.7
2	B	1488	ASN	2.7
1	I	129	ARG	2.6
1	I	136	THR	2.6
1	I	39	GLU	2.6
1	I	112	HIS	2.6
1	I	32	THR	2.5
1	I	43	THR	2.5
1	I	151	ILE	2.5
2	C	1632	THR	2.5
2	E	1500	VAL	2.5
2	E	1841	ILE	2.4
1	I	133	ALA	2.3
2	B	1485	LEU	2.3
2	B	1589	THR	2.3
1	I	127	ASP	2.3
1	I	154	SER	2.3
1	I	107	LYS	2.2
1	I	167	THR	2.2
1	I	68	ALA	2.1
2	B	1524	ASP	2.1
2	E	1711[A]	TRP	2.1
1	I	50	THR	2.1
2	B	1471	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	I	132	ARG	2.1
1	I	109	LEU	2.1
2	C	1808	ASP	2.1
1	I	36	PHE	2.1
1	I	48	PHE	2.1
2	B	1477	TYR	2.1
1	I	47	GLU	2.0
1	I	140	ARG	2.0
2	B	1489	LEU	2.0
2	B	1849	PHE	2.0
2	B	1664	ARG	2.0
1	I	63	GLN	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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.

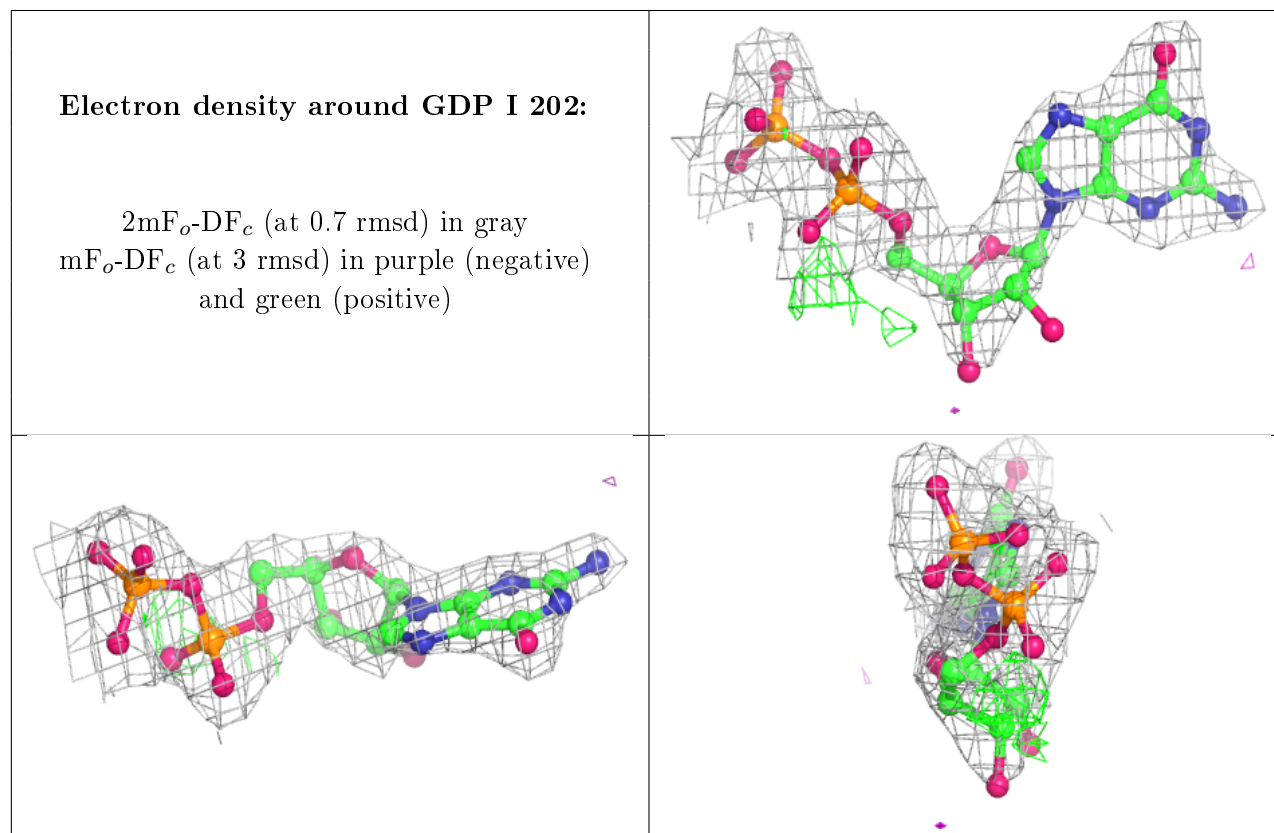
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	EDO	C	1902	4/4	0.62	0.32	74,82,86,89	0
8	GOL	B	1903	6/6	0.75	0.20	64,74,77,83	0
5	BEF	I	203	4/4	0.77	0.21	40,40,40,41	4
8	GOL	A	208	6/6	0.79	0.14	59,78,84,87	0
3	MG	I	201	1/1	0.82	0.07	42,42,42,42	1
6	EDO	E	1901	4/4	0.84	0.21	45,57,60,67	0
6	EDO	C	1904	4/4	0.86	0.31	34,48,65,69	0
3	MG	C	1905	1/1	0.86	0.24	85,85,85,85	0
6	EDO	B	1901	4/4	0.89	0.23	56,59,62,63	0
6	EDO	A	205	4/4	0.90	0.17	47,63,67,73	0
7	ACT	A	207	4/4	0.90	0.17	47,64,69,71	0

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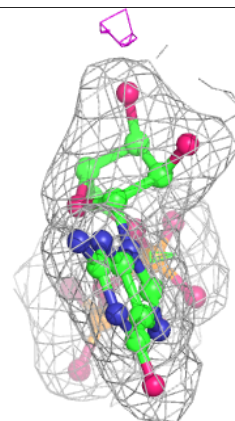
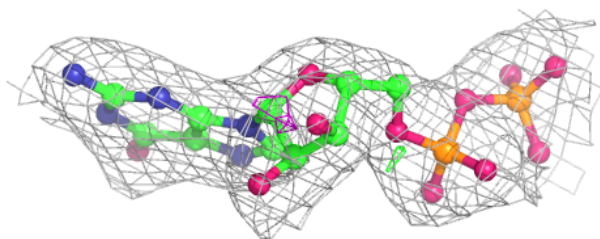
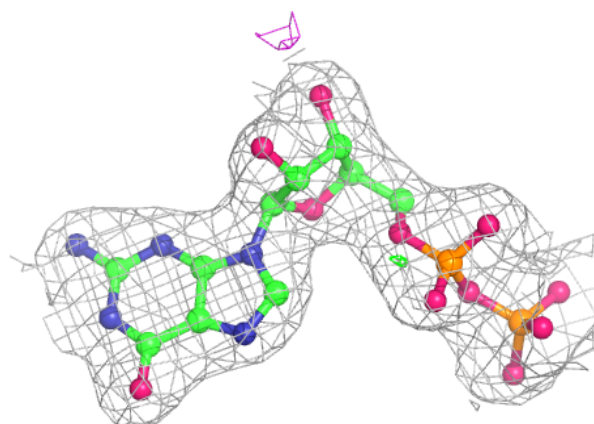
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GDP	I	202	28/28	0.90	0.20	31,45,54,66	28
6	EDO	B	1902	4/4	0.91	0.18	56,57,58,65	0
6	EDO	E	1902	4/4	0.91	0.19	48,51,57,57	0
6	EDO	D	205	4/4	0.93	0.13	56,58,60,61	0
6	EDO	C	1903	4/4	0.93	0.12	56,57,65,71	0
5	BEF	D	203	4/4	0.93	0.08	46,46,49,49	0
5	BEF	A	203	4/4	0.94	0.10	38,40,40,43	0
6	EDO	A	206	4/4	0.94	0.15	48,49,51,66	0
7	ACT	C	1906	4/4	0.94	0.11	59,61,65,69	0
6	EDO	D	204	4/4	0.95	0.25	67,68,71,80	0
3	MG	D	201	1/1	0.96	0.11	47,47,47,47	0
6	EDO	A	204	4/4	0.97	0.13	42,44,45,46	0
6	EDO	C	1901	4/4	0.98	0.13	44,45,53,60	0
4	GDP	D	202	28/28	0.98	0.11	41,47,51,53	0
3	MG	A	201	1/1	0.98	0.04	43,43,43,43	0
4	GDP	A	202	28/28	0.98	0.12	35,39,43,44	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.

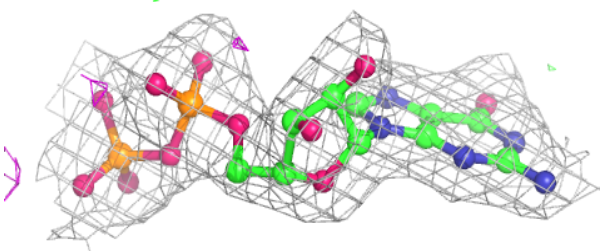
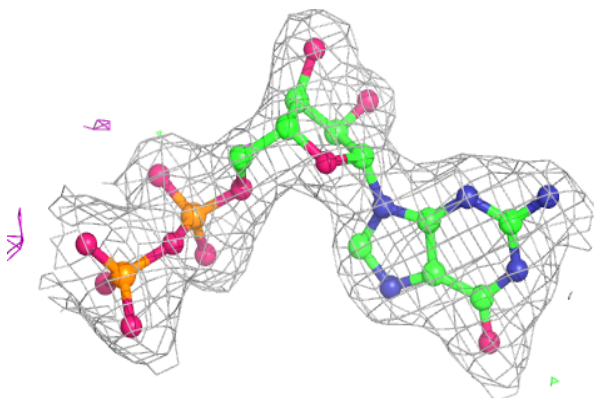


Electron density around GDP D 202:

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

**Electron density around GDP A 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.