



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 19, 2023 – 04:04 PM EDT

PDB ID : 2H7V
Title : Co-crystal structure of YpkA-Rac1
Authors : Prehna, G.; Ivanov, M.; Bliska, J.B.; Stebbins, C.E.
Deposited on : 2006-06-04
Resolution : 2.60 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

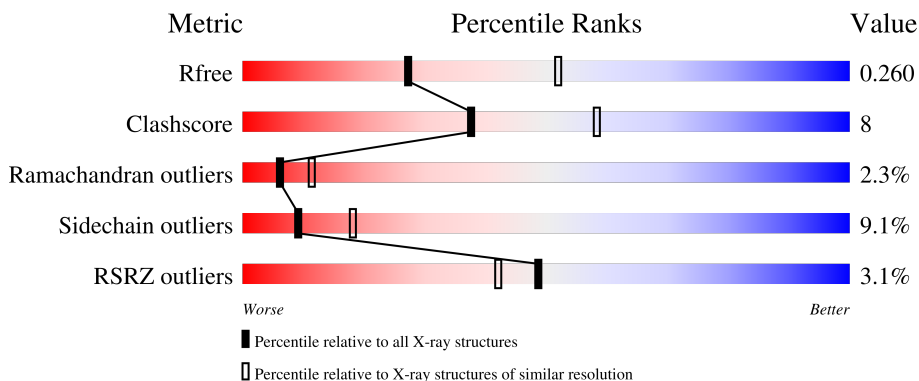
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	188	 % 79% 15% . .
1	B	188	 % 82% 12% . . .
2	C	303	 % 64% 21% . 11%
2	D	303	 7% 58% 23% . . 15%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 7191 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 Migration-inducing protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	182	1411	903	234	265	9	0	0	0
1	B	183	1418	908	235	266	9	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1B	GLY	-	cloning artifact	UNP P63000
A	2B	SER	-	cloning artifact	UNP P63000
A	1A	LYS	-	cloning artifact	UNP P63000
A	2A	LEU	-	cloning artifact	UNP P63000
A	78	SER	PHE	engineered mutation	UNP P63000
B	1B	GLY	-	cloning artifact	UNP P63000
B	2B	SER	-	cloning artifact	UNP P63000
B	1A	LYS	-	cloning artifact	UNP P63000
B	2A	LEU	-	cloning artifact	UNP P63000
B	78	SER	PHE	engineered mutation	UNP P63000

- Molecule 2 is a protein called Protein kinase ypkA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	269	2151	1339	388	416	8	0	0	0
2	D	259	2078	1293	374	404	7	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	430	GLY	-	cloning artifact	UNP Q05608
C	431	PRO	-	cloning artifact	UNP Q05608

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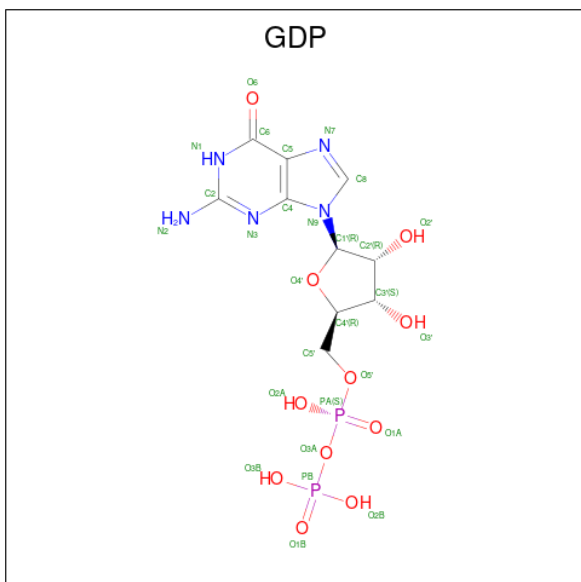
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Chain	Residue	Modelled	Actual	Comment	Reference
C	432	VAL	-	cloning artifact	UNP Q05608
C	433	ASP	-	cloning artifact	UNP Q05608
D	430	GLY	-	cloning artifact	UNP Q05608
D	431	PRO	-	cloning artifact	UNP Q05608
D	432	VAL	-	cloning artifact	UNP Q05608
D	433	ASP	-	cloning artifact	UNP Q05608

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

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

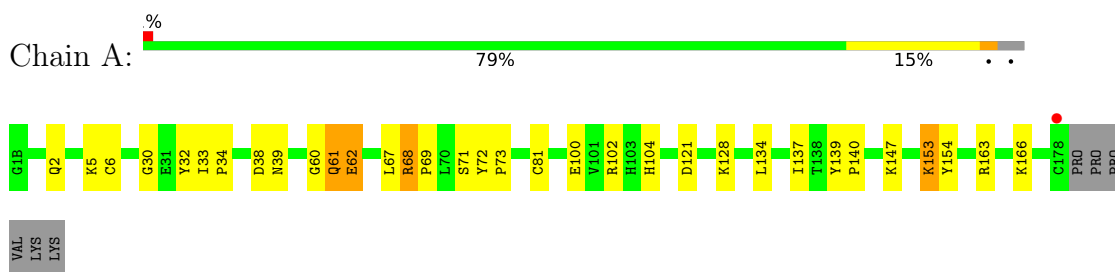
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	9	Total O 9 9	0	0
5	B	10	Total O 10 10	0	0
5	C	32	Total O 32 32	0	0
5	D	24	Total O 24 24	0	0

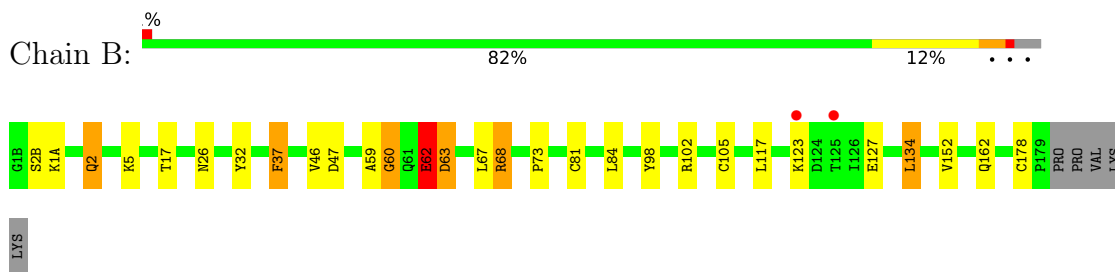
3 Residue-property plots [i](#)

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

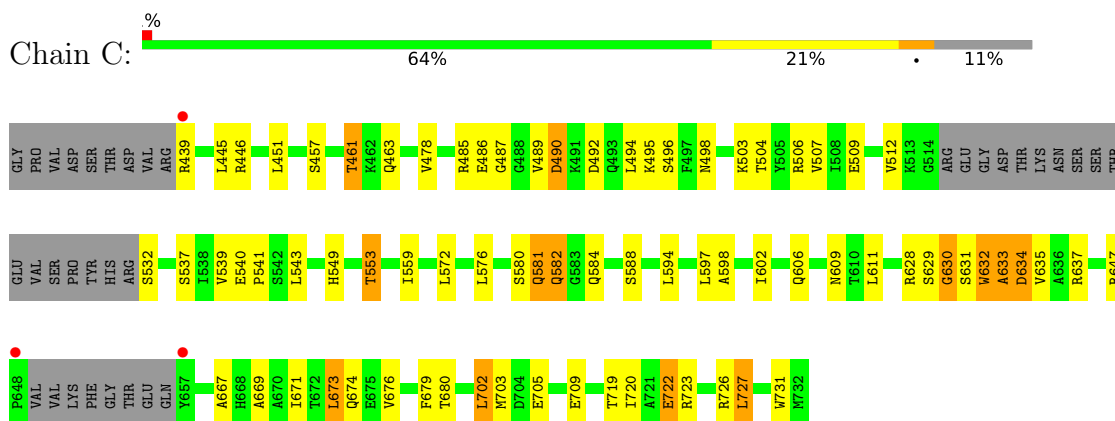
- Molecule 1: Migration-inducing protein 5



- Molecule 1: Migration-inducing protein 5

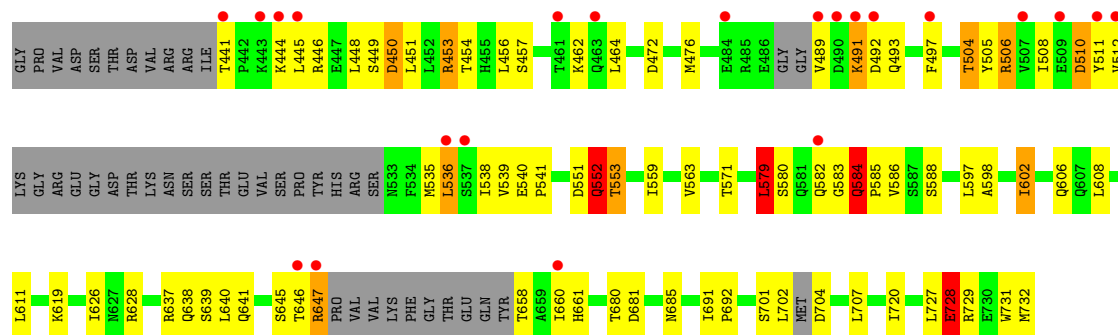


- Molecule 2: Protein kinase ypkA



- Molecule 2: Protein kinase ypkA





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.40Å 75.52Å 99.77Å 92.08° 103.38° 115.79°	Depositor
Resolution (Å)	95.78 – 2.60 34.86 – 2.58	Depositor EDS
% Data completeness (in resolution range)	99.4 (95.78-2.60) 98.3 (34.86-2.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 2.57Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.222 , 0.257 0.226 , 0.260	Depositor DCC
R_{free} test set	2588 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	62.0	Xtrriage
Anisotropy	0.564	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 61.9	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	0.95	EDS
Total number of atoms	7191	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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: MG, GDP

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	0.77	2/1440 (0.1%)	0.85	2/1957 (0.1%)
1	B	0.81	4/1448 (0.3%)	0.80	2/1969 (0.1%)
2	C	0.91	4/2176 (0.2%)	0.85	2/2928 (0.1%)
2	D	0.73	2/2099 (0.1%)	0.80	1/2823 (0.0%)
All	All	0.81	12/7163 (0.2%)	0.82	7/9677 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	2
2	D	0	2
All	All	0	4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	630	GLY	N-CA	-8.28	1.33	1.46
2	C	629	SER	C-O	8.08	1.38	1.23
2	D	728	GLU	CG-CD	7.10	1.62	1.51
1	B	81	CYS	CB-SG	-6.89	1.70	1.82
1	B	62	GLU	CG-CD	6.88	1.62	1.51
1	B	105	CYS	CB-SG	-6.74	1.70	1.82
2	D	728	GLU	CB-CG	6.14	1.63	1.52
1	B	62	GLU	CB-CG	5.85	1.63	1.52
2	C	632	TRP	CE3-CZ3	5.65	1.48	1.38
1	A	81	CYS	CB-SG	-5.36	1.73	1.81
1	A	6	CYS	CB-SG	-5.18	1.73	1.81
2	C	722	GLU	CG-CD	5.17	1.59	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	68	ARG	NE-CZ-NH2	-9.01	115.80	120.30
1	A	68	ARG	NE-CZ-NH1	7.49	124.05	120.30
1	B	134	LEU	CA-CB-CG	7.04	131.49	115.30
2	C	628	ARG	NE-CZ-NH1	6.08	123.34	120.30
2	C	637	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	B	68	ARG	NE-CZ-NH1	5.10	122.85	120.30
2	D	579	LEU	CA-CB-CG	5.08	126.98	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	485	ARG	Peptide
2	C	630	GLY	Peptide
2	D	551	ASP	Peptide
2	D	552	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1411	0	1438	15	0
1	B	1418	0	1445	11	0
2	C	2151	0	2187	41	0
2	D	2078	0	2109	44	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	28	0	12	0	0
4	B	28	0	12	0	0
5	A	9	0	0	2	0
5	B	10	0	0	0	0
5	C	32	0	0	9	0
5	D	24	0	0	3	0
All	All	7191	0	7203	110	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 8.

All (110) 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:D:606:GLN:HB2	5:D:2:HOH:O	1.82	0.80
1:B:98:TYR:CE1	1:B:102:ARG:HD2	2.17	0.79
2:C:559:ILE:HD13	2:C:611:LEU:HD23	1.65	0.79
1:B:5:LYS:NZ	1:B:73:PRO:O	2.22	0.73
2:D:658:THR:OG1	2:D:661:HIS:ND1	2.19	0.72
1:B:26:ASN:HA	1:B:162:GLN:HE22	1.54	0.71
2:C:609:ASN:ND2	5:C:53:HOH:O	2.24	0.69
2:C:486:GLU:HB2	5:C:28:HOH:O	1.93	0.68
2:C:669:ALA:HB1	2:C:727:LEU:HD13	1.76	0.67
2:C:722:GLU:O	2:C:726:ARG:HG2	1.94	0.66
2:C:634:ASP:HA	5:C:52:HOH:O	1.96	0.65
2:D:728:GLU:HG2	5:D:23:HOH:O	1.98	0.64
2:D:645:SER:O	2:D:647:ARG:HD2	1.98	0.64
2:D:701:SER:O	2:D:702:LEU:HD23	1.98	0.64
2:D:702:LEU:O	2:D:704:ASP:N	2.32	0.62
1:A:5:LYS:NZ	1:A:71:SER:O	2.31	0.62
2:D:579:LEU:O	2:D:583:GLY:N	2.32	0.62
2:C:581:GLN:O	2:C:582:GLN:HB3	2.00	0.61
2:C:635:VAL:HG12	2:C:676:VAL:HG12	1.82	0.61
2:C:709:GLU:OE1	5:C:30:HOH:O	2.16	0.61
2:C:487:GLY:C	2:C:489:VAL:H	2.04	0.61
2:D:563:VAL:HG22	2:D:608:LEU:HD21	1.84	0.60
2:C:631:SER:HB3	5:C:68:HOH:O	2.01	0.60
2:D:579:LEU:HD23	2:D:580:SER:N	2.17	0.60
2:C:503:LYS:O	2:C:507:VAL:HG23	2.03	0.58
2:D:598:ALA:O	2:D:602:ILE:HG23	2.04	0.57
2:C:673:LEU:HD13	2:C:727:LEU:HD12	1.87	0.56
2:C:702:LEU:O	2:C:703:MET:HG2	2.07	0.55
2:D:489:VAL:HG13	2:D:491:LYS:HD3	1.89	0.54
1:A:60:GLY:O	1:A:61:GLN:HG3	2.07	0.54
2:C:631:SER:CB	5:C:68:HOH:O	2.56	0.54
2:D:489:VAL:HG13	2:D:491:LYS:CD	2.38	0.54
1:A:139:TYR:HB3	1:A:140:PRO:HD3	1.89	0.54
2:C:580:SER:O	2:C:582:GLN:N	2.41	0.54
2:C:632:TRP:CE3	2:C:633:ALA:N	2.76	0.53
2:D:506:ARG:HG3	2:D:510:ASP:OD1	2.09	0.53
2:D:658:THR:N	5:D:32:HOH:O	2.42	0.53
1:A:2:GLN:NE2	5:A:202:HOH:O	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:559:ILE:HG12	2:D:611:LEU:HD23	1.91	0.52
2:C:679:PHE:O	2:C:680:THR:C	2.48	0.52
2:C:543:LEU:HD13	2:C:597:LEU:HD12	1.91	0.52
2:D:619:LYS:HG2	2:D:707:LEU:HD13	1.93	0.51
1:B:59:ALA:O	1:B:60:GLY:C	2.50	0.50
2:D:619:LYS:HG2	2:D:707:LEU:CD1	2.41	0.50
2:C:634:ASP:CA	5:C:52:HOH:O	2.56	0.50
2:C:727:LEU:HD22	2:C:731:TRP:HD1	1.77	0.50
2:C:509:GLU:O	2:C:512:VAL:HG22	2.13	0.48
2:D:505:TYR:HD1	2:D:571:THR:HG21	1.79	0.48
1:B:123:LYS:HZ1	1:B:127:GLU:HG3	1.77	0.48
2:C:598:ALA:O	2:C:602:ILE:HG23	2.14	0.48
1:A:61:GLN:HA	5:A:207:HOH:O	2.14	0.48
2:C:634:ASP:CB	5:C:52:HOH:O	2.61	0.47
2:D:472:ASP:O	2:D:476:MET:HG2	2.14	0.47
1:B:62:GLU:O	1:B:63:ASP:HB2	2.14	0.47
2:D:691:ILE:HB	2:D:692:PRO:HD3	1.95	0.47
2:C:553:THR:HA	5:C:3:HOH:O	2.14	0.47
2:D:445:LEU:HA	2:D:448:LEU:HD12	1.97	0.47
2:D:645:SER:O	2:D:647:ARG:CD	2.62	0.47
1:A:137:ILE:HD12	1:A:137:ILE:N	2.30	0.46
2:D:450:ASP:HA	2:D:453:ARG:HB2	1.96	0.46
2:D:640:LEU:HD23	2:D:720:ILE:HD12	1.98	0.46
1:A:100:GLU:O	1:A:104:HIS:HD2	1.99	0.46
2:C:539:VAL:HG13	2:C:572:LEU:HD13	1.98	0.45
2:D:508:ILE:HG23	2:D:512:VAL:HG11	1.98	0.45
2:D:535:MET:HA	2:D:539:VAL:HG22	1.97	0.45
2:D:552:GLN:HG3	2:D:553:THR:H	1.81	0.45
1:B:2:GLN:HE21	1:B:2:GLN:HB3	1.56	0.45
2:C:492:ASP:O	2:C:495:LYS:HG2	2.17	0.45
2:C:490:ASP:O	2:C:494:LEU:HD23	2.17	0.44
2:C:632:TRP:CE3	2:C:632:TRP:C	2.91	0.44
2:D:638:GLN:O	2:D:639:SER:C	2.56	0.44
2:C:540:GLU:N	2:C:541:PRO:HD2	2.31	0.44
2:D:453:ARG:HH12	2:D:456:LEU:HD22	1.83	0.44
1:A:68:ARG:N	1:A:69:PRO:HD2	2.33	0.44
1:B:46:VAL:O	1:B:47:ASP:C	2.56	0.44
1:A:60:GLY:O	1:A:61:GLN:CG	2.66	0.44
1:B:84:LEU:HD12	1:B:117:LEU:HA	1.99	0.44
1:A:33:ILE:O	1:A:34:PRO:C	2.54	0.43
1:B:98:TYR:CZ	1:B:102:ARG:HD2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:506:ARG:O	2:D:510:ASP:N	2.46	0.43
2:D:511:TYR:O	2:D:512:VAL:HG13	2.18	0.43
2:C:719:THR:O	2:C:723:ARG:HG2	2.19	0.43
2:D:536:LEU:O	2:D:540:GLU:HB2	2.18	0.43
2:D:508:ILE:CG2	2:D:512:VAL:HG11	2.48	0.43
2:C:559:ILE:CD1	2:C:611:LEU:HD23	2.43	0.43
2:D:645:SER:O	2:D:647:ARG:N	2.52	0.43
2:D:584:GLN:O	2:D:586:VAL:N	2.52	0.42
2:D:464:LEU:H	2:D:464:LEU:HD23	1.84	0.42
1:B:17:THR:HG23	1:B:37:PHE:HB2	2.00	0.42
1:A:68:ARG:HD2	1:A:100:GLU:OE2	2.19	0.42
2:C:667:ALA:O	2:C:671:ILE:HG12	2.19	0.42
2:C:487:GLY:C	2:C:489:VAL:N	2.72	0.42
1:A:72:TYR:N	1:A:73:PRO:CD	2.83	0.42
2:C:461:THR:O	2:C:463:GLN:NE2	2.51	0.42
1:A:39:ASN:ND2	2:C:588:SER:HB2	2.35	0.42
2:C:445:LEU:HD22	2:C:489:VAL:HG11	2.02	0.41
2:D:727:LEU:HD22	2:D:731:TRP:CD1	2.56	0.41
2:D:637:ARG:O	2:D:641:GLN:HG3	2.19	0.41
1:A:61:GLN:HB3	1:A:62:GLU:OE2	2.20	0.41
1:A:153:LYS:CE	1:A:154:TYR:H	2.33	0.41
2:D:540:GLU:N	2:D:541:PRO:CD	2.83	0.41
2:D:552:GLN:CG	2:D:553:THR:H	2.34	0.41
2:C:602:ILE:O	2:C:606:GLN:HG3	2.20	0.40
2:C:581:GLN:O	2:C:582:GLN:CB	2.69	0.40
2:C:540:GLU:N	2:C:541:PRO:CD	2.83	0.40
2:C:576:LEU:HB3	2:C:594:LEU:HD21	2.04	0.40
2:D:491:LYS:C	2:D:493:GLN:H	2.25	0.40
2:D:504:THR:O	2:D:505:TYR:C	2.60	0.40
2:D:505:TYR:CD1	2:D:571:THR:HG21	2.55	0.40
2:D:538:ILE:HG22	2:D:539:VAL:HG13	2.02	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	180/188 (96%)	170 (94%)	6 (3%)	4 (2%)	6	12
1	B	181/188 (96%)	163 (90%)	13 (7%)	5 (3%)	5	7
2	C	263/303 (87%)	238 (90%)	21 (8%)	4 (2%)	10	21
2	D	249/303 (82%)	228 (92%)	14 (6%)	7 (3%)	5	7
All	All	873/982 (89%)	799 (92%)	54 (6%)	20 (2%)	6	11

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	TYR
1	A	61	GLN
1	B	32	TYR
1	B	60	GLY
2	C	581	GLN
2	D	585	PRO
2	D	646	THR
1	B	63	ASP
2	C	582	GLN
2	D	552	GLN
1	B	2(B)	SER
2	D	492	ASP
1	A	62	GLU
2	D	553	THR
1	B	1(A)	LYS
2	C	584	GLN
2	C	633	ALA
2	D	536	LEU
1	A	30	GLY
2	D	584	GLN

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	157/163 (96%)	147 (94%)	10 (6%)	17	35
1	B	158/163 (97%)	150 (95%)	8 (5%)	24	46
2	C	242/273 (89%)	219 (90%)	23 (10%)	8	16
2	D	235/273 (86%)	204 (87%)	31 (13%)	4	7
All	All	792/872 (91%)	720 (91%)	72 (9%)	9	18

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	ASP
1	A	67	LEU
1	A	102	ARG
1	A	121	ASP
1	A	128	LYS
1	A	134	LEU
1	A	147	LYS
1	A	153	LYS
1	A	163	ARG
1	A	166	LYS
1	B	2	GLN
1	B	37	PHE
1	B	62	GLU
1	B	67	LEU
1	B	68	ARG
1	B	134	LEU
1	B	152	VAL
1	B	178	CYS
2	C	439	ARG
2	C	446	ARG
2	C	451	LEU
2	C	457	SER
2	C	461	THR
2	C	478	VAL
2	C	490	ASP
2	C	496	SER
2	C	498	ASN
2	C	504	THR
2	C	506	ARG
2	C	532	SER
2	C	537	SER
2	C	549	HIS
2	C	553	THR

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Mol	Chain	Res	Type
2	C	634	ASP
2	C	647	ARG
2	C	673	LEU
2	C	674	GLN
2	C	702	LEU
2	C	705	GLU
2	C	720	ILE
2	C	727	LEU
2	D	441	THR
2	D	444	LYS
2	D	446	ARG
2	D	449	SER
2	D	450	ASP
2	D	451	LEU
2	D	453	ARG
2	D	454	THR
2	D	457	SER
2	D	462	LYS
2	D	491	LYS
2	D	497	PHE
2	D	504	THR
2	D	506	ARG
2	D	510	ASP
2	D	579	LEU
2	D	582	GLN
2	D	584	GLN
2	D	588	SER
2	D	597	LEU
2	D	602	ILE
2	D	626	ILE
2	D	628	ARG
2	D	647	ARG
2	D	660	ILE
2	D	680	THR
2	D	681	ASP
2	D	685	ASN
2	D	728	GLU
2	D	729	ARG
2	D	732	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	HIS
1	A	162	GLN
1	B	2	GLN
1	B	43	ASN
1	B	52	ASN
1	B	61	GLN
1	B	162	GLN
2	C	493	GLN
2	C	498	ASN
2	C	544	GLN
2	C	552	GLN
2	C	554	HIS
2	C	581	GLN
2	C	627	ASN
2	C	668	HIS
2	C	696	GLN
2	C	706	HIS
2	D	533	ASN
2	D	581	GLN
2	D	584	GLN
2	D	612	GLN
2	D	615	GLN
2	D	685	ASN
2	D	696	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GDP	A	200	3	24,30,30	1.10	1 (4%)	30,47,47	1.40	4 (13%)
4	GDP	B	200	3	24,30,30	0.95	1 (4%)	30,47,47	1.59	7 (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	GDP	A	200	3	-	5/12/32/32	0/3/3/3
4	GDP	B	200	3	-	3/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	200	GDP	C6-N1	-3.18	1.33	1.37
4	B	200	GDP	C6-N1	-2.23	1.34	1.37

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	200	GDP	PA-O3A-PB	-4.20	118.40	132.83
4	B	200	GDP	PA-O3A-PB	-3.15	122.03	132.83
4	B	200	GDP	C3'-C2'-C1'	3.10	105.65	100.98
4	B	200	GDP	C5-C6-N1	2.69	118.70	113.95
4	A	200	GDP	O2B-PB-O1B	-2.65	100.31	110.68
4	B	200	GDP	O3B-PB-O2B	2.64	117.73	107.64
4	B	200	GDP	C8-N7-C5	2.42	107.60	102.99
4	A	200	GDP	C8-N7-C5	2.29	107.36	102.99
4	B	200	GDP	O2A-PA-O5'	2.18	117.88	107.75
4	B	200	GDP	O5'-C5'-C4'	-2.12	101.68	108.99
4	A	200	GDP	O2B-PB-O3A	2.10	111.68	104.64

There are no chirality outliers.

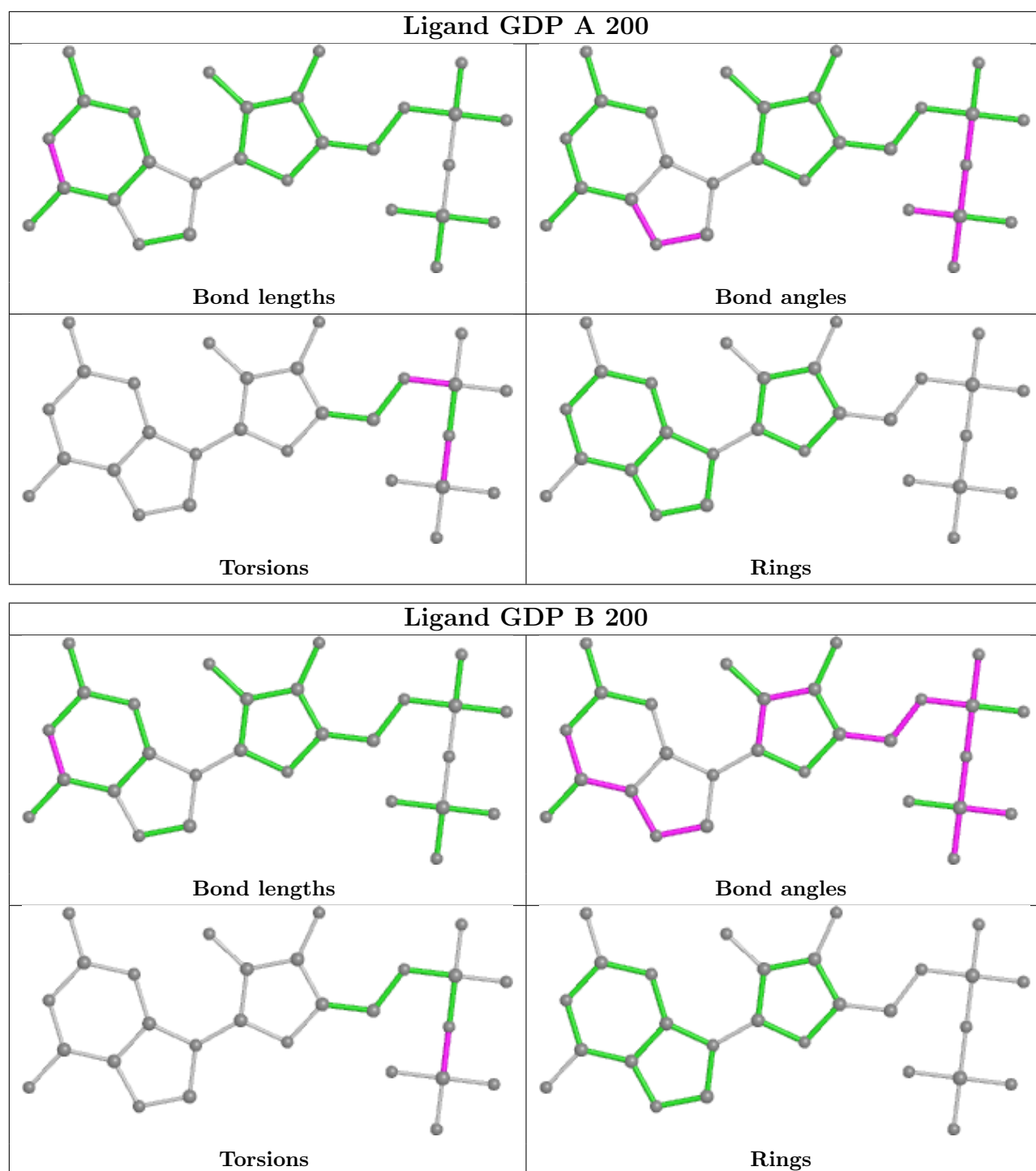
All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	200	GDP	PA-O3A-PB-O3B
4	A	200	GDP	C5'-O5'-PA-O3A
4	B	200	GDP	PA-O3A-PB-O3B
4	A	200	GDP	PA-O3A-PB-O2B
4	B	200	GDP	PA-O3A-PB-O2B
4	A	200	GDP	C5'-O5'-PA-O2A
4	B	200	GDP	PA-O3A-PB-O1B
4	A	200	GDP	C5'-O5'-PA-O1A

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.



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	182/188 (96%)	-0.07	1 (0%) 91 89	51, 67, 76, 86	0
1	B	183/188 (97%)	-0.06	2 (1%) 80 78	41, 65, 74, 85	0
2	C	269/303 (88%)	-0.07	3 (1%) 80 78	31, 62, 80, 84	0
2	D	259/303 (85%)	0.28	22 (8%) 10 7	49, 66, 82, 86	0
All	All	893/982 (90%)	0.03	28 (3%) 49 42	31, 65, 80, 86	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	511	TYR	6.2
2	D	646	THR	5.8
2	C	657	TYR	4.0
2	D	509	GLU	4.0
2	D	441	THR	3.7
1	B	125	THR	3.5
2	D	490	ASP	3.4
2	D	445	LEU	3.4
2	D	492	ASP	3.4
2	D	489	VAL	3.2
1	A	178	CYS	3.1
2	D	582	GLN	3.0
2	C	648	PRO	2.9
2	D	507	VAL	2.8
2	D	443	LYS	2.8
2	D	536	LEU	2.7
2	D	491	LYS	2.6
2	D	463	GLN	2.5
2	D	512	VAL	2.5
2	D	497	PHE	2.5
2	D	537	SER	2.5

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Mol	Chain	Res	Type	RSRZ
2	C	439	ARG	2.4
2	D	660	ILE	2.4
1	B	123	LYS	2.3
2	D	647	ARG	2.3
2	D	461	THR	2.2
2	D	444	LYS	2.1
2	D	484	GLU	2.1

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

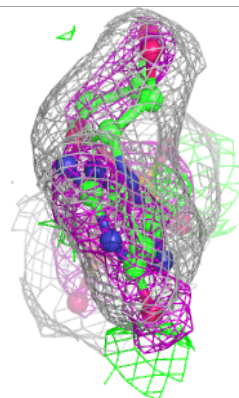
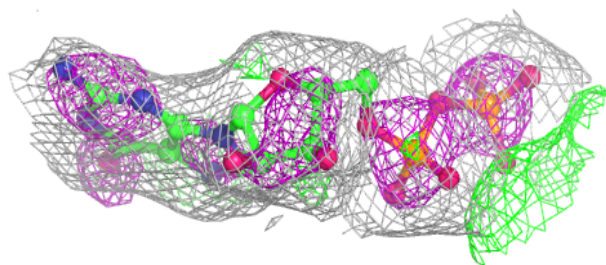
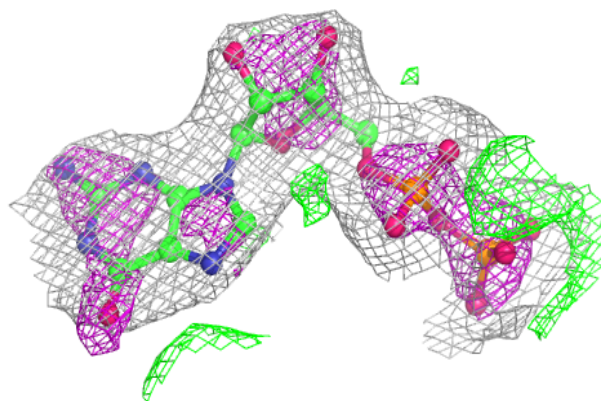
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	B	201	1/1	0.93	0.23	63,63,63,63	0
4	GDP	B	200	28/28	0.95	0.11	58,79,79,82	0
4	GDP	A	200	28/28	0.97	0.10	50,74,77,77	0
3	MG	A	201	1/1	0.98	0.22	49,49,49,49	0

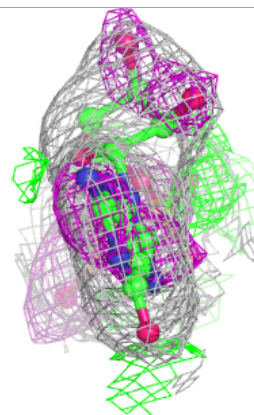
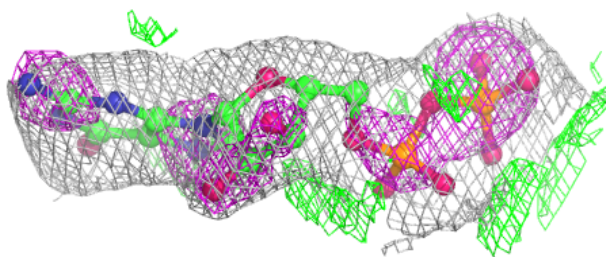
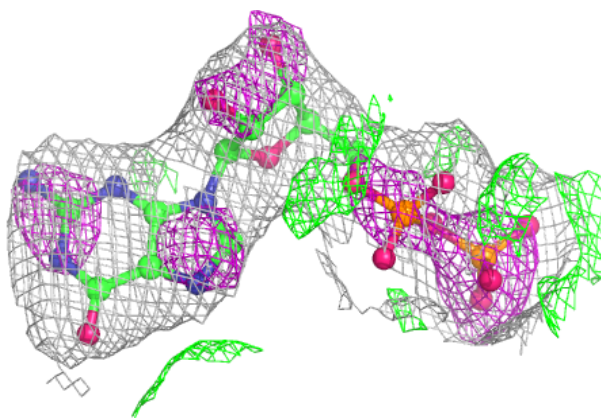
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GDP B 200:

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

**Electron density around GDP A 200:**

$2mF_o-DF_c$ (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.