



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 11:08 am BST

PDB ID : 3C50
Title : Crystal Structure of G protein coupled receptor kinase 1 bound to ADP and magnesium chloride at 2.6Å
Authors : Singh, P.; Tesmer, J.J.G.
Deposited on : 2008-01-30
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 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

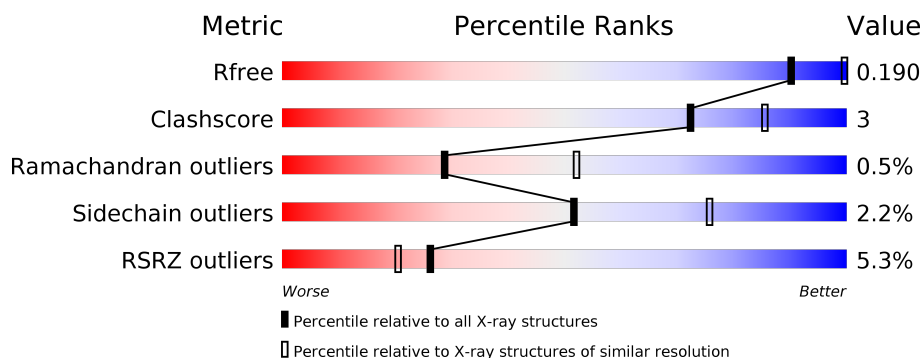
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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 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	543	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>10%</div> <div>8%</div> </div> </div>
1	B	543	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>6%</div> <div>9%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8438 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 Rhodopsin kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	4	0
			4041	2591	699	732	19			
1	B	496	Total	C	N	O	S	0	4	0
			4016	2578	693	726	19			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	536	VAL	-	EXPRESSION TAG	UNP P28327
A	537	ASP	-	EXPRESSION TAG	UNP P28327
A	538	HIS	-	EXPRESSION TAG	UNP P28327
A	539	HIS	-	EXPRESSION TAG	UNP P28327
A	540	HIS	-	EXPRESSION TAG	UNP P28327
A	541	HIS	-	EXPRESSION TAG	UNP P28327
A	542	HIS	-	EXPRESSION TAG	UNP P28327
A	543	HIS	-	EXPRESSION TAG	UNP P28327
B	536	VAL	-	EXPRESSION TAG	UNP P28327
B	537	ASP	-	EXPRESSION TAG	UNP P28327
B	538	HIS	-	EXPRESSION TAG	UNP P28327
B	539	HIS	-	EXPRESSION TAG	UNP P28327
B	540	HIS	-	EXPRESSION TAG	UNP P28327
B	541	HIS	-	EXPRESSION TAG	UNP P28327
B	542	HIS	-	EXPRESSION TAG	UNP P28327
B	543	HIS	-	EXPRESSION TAG	UNP P28327

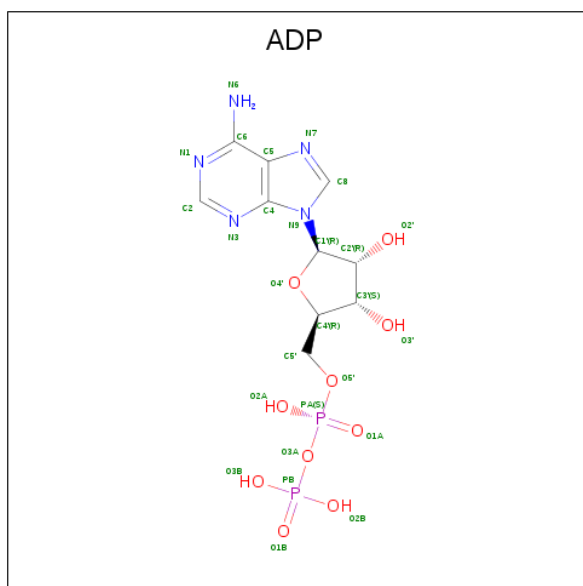
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	5	Total	Cl	0	0
			5	5		
3	A	3	Total	Cl	0	0
			3	3		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

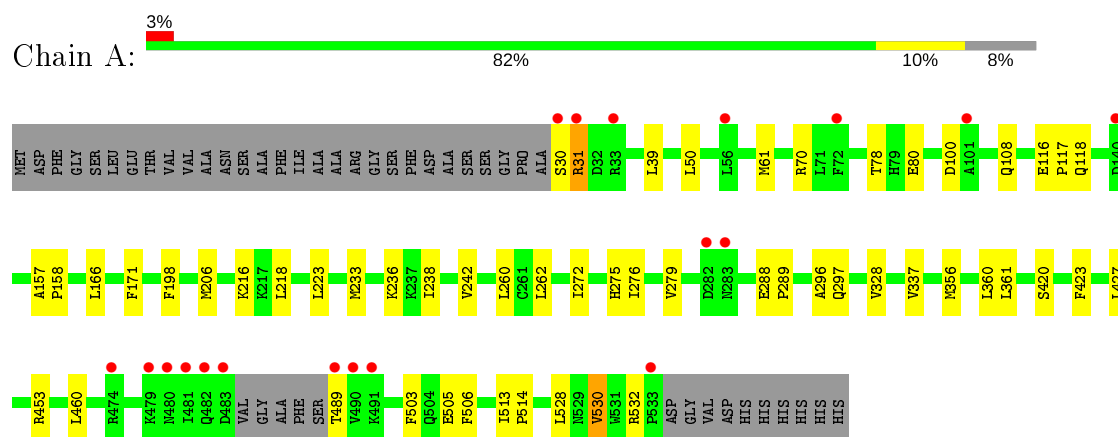
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	165	Total	O	0	0
			165	165		
6	B	138	Total	O	0	0
			138	138		

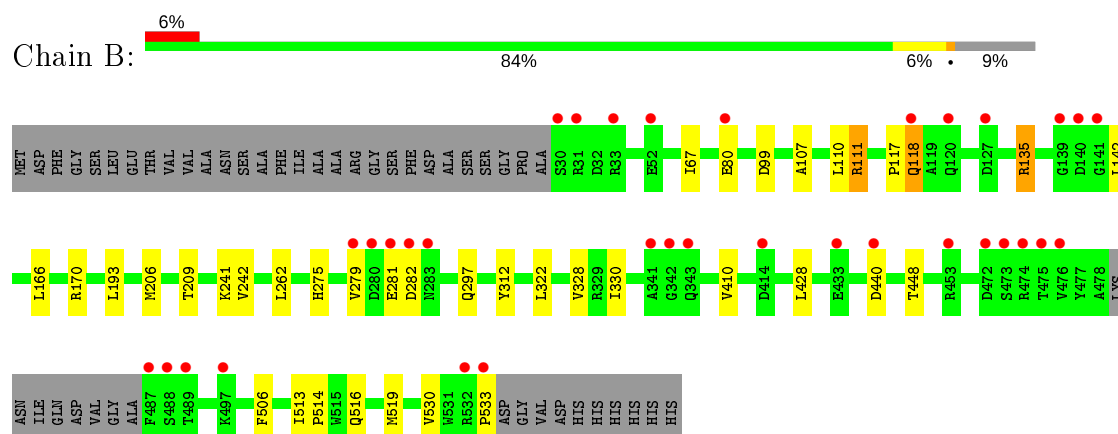
3 Residue-property plots [i](#)

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: Rhodopsin kinase



• Molecule 1: Rhodopsin kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.50Å 122.30Å 174.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60 19.88 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.60) 99.8 (19.88-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 2.59Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , (Not available) 0.192 , 0.190	Depositor DCC
R_{free} test set	2196 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8438	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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

5.1 Standard geometry

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

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	0.53	0/4137	0.64	0/5581
1	B	0.51	0/4113	0.61	0/5549
All	All	0.52	0/8250	0.63	0/11130

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

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	4041	0	4006	32	0
1	B	4016	0	3978	28	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	3	0	0	0	0
3	B	5	0	0	0	0
4	A	27	0	12	0	0
4	B	27	0	12	1	0
5	A	12	0	12	0	0
6	A	165	0	0	2	0
6	B	138	0	0	3	0
All	All	8438	0	8020	55	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 3.

All (55) 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:530:VAL:HG23	6:A:687:HOH:O	1.62	0.99
1:B:117[B]:PRO:O	1:B:118[B]:GLN:HB2	1.83	0.77
1:B:117[B]:PRO:O	1:B:118[B]:GLN:CB	2.34	0.74
1:A:356:MET:HE2	1:A:361:LEU:HD21	1.74	0.68
1:B:448:THR:HG22	1:B:448:THR:O	1.95	0.66
1:A:117[B]:PRO:O	1:A:118[B]:GLN:HB2	1.99	0.63
1:A:78:THR:HG22	1:B:533:PRO:HD3	1.82	0.61
1:A:532:ARG:NH2	1:B:530:VAL:HG12	2.16	0.60
1:B:242:VAL:HG23	6:B:598:HOH:O	2.03	0.59
1:A:39:LEU:O	1:A:528:LEU:HD11	2.03	0.58
1:A:275:HIS:HA	1:A:279:VAL:HG23	1.85	0.58
1:B:142:LEU:O	6:B:677:HOH:O	2.16	0.58
1:B:448:THR:O	1:B:448:THR:CG2	2.53	0.56
1:B:312:TYR:CZ	1:B:330[B]:ILE:HG23	2.41	0.56
1:A:117[B]:PRO:O	1:A:118[B]:GLN:CB	2.55	0.55
1:A:242:VAL:HG23	6:A:600:HOH:O	2.08	0.54
1:A:238:ILE:O	1:A:242:VAL:HG22	2.08	0.53
1:B:67:ILE:HD12	1:B:516:GLN:HG2	1.90	0.53
1:B:193:LEU:HD13	4:B:562:ADP:C2	2.43	0.53
1:B:117[B]:PRO:O	1:B:118[B]:GLN:CG	2.57	0.52
1:A:297:GLN:OE1	1:A:328:VAL:HG22	2.09	0.52
1:B:117[B]:PRO:O	1:B:118[B]:GLN:HG2	2.10	0.52
1:B:107:ALA:O	1:B:111:ARG:HG3	2.09	0.51
1:B:322:LEU:HG	1:B:328:VAL:HG12	1.93	0.51
1:B:410:VAL:HG21	1:B:428:LEU:HD13	1.92	0.51
1:B:242:VAL:CG2	6:B:598:HOH:O	2.60	0.48
1:A:260:LEU:HD21	1:A:503:PHE:CD2	2.49	0.48
1:A:356:MET:CE	1:A:361:LEU:HD21	2.42	0.47
1:B:110:LEU:HD23	1:B:110:LEU:C	2.35	0.47
1:A:262:LEU:HD21	1:A:506:PHE:CZ	2.49	0.47
1:A:216:LYS:HE2	1:A:218:LEU:HD21	1.97	0.47
1:A:423:PHE:CE2	1:A:427:LEU:HD11	2.51	0.46
1:B:262:LEU:HD21	1:B:506:PHE:CZ	2.51	0.46
1:A:166:LEU:HD22	1:B:166:LEU:HD22	1.98	0.46
1:A:513:ILE:HB	1:A:514:PRO:HD3	1.98	0.45
1:B:135:ARG:O	1:B:135:ARG:HG3	2.16	0.45
1:A:288:GLU:HB3	1:A:289:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:LEU:HD23	1:A:360:LEU:C	2.37	0.45
1:A:30:SER:O	1:A:31:ARG:C	2.57	0.43
1:A:236:LYS:HG3	1:A:262:LEU:HD21	2.01	0.43
1:A:296:ALA:HB1	1:A:460:LEU:HD22	2.01	0.43
1:A:61:MET:HG3	1:A:171:PHE:CE2	2.54	0.43
1:A:198:PHE:CE2	1:A:223:LEU:HD23	2.54	0.43
1:A:157:ALA:HB3	1:A:158:PRO:HD3	2.01	0.42
1:B:209:THR:HG21	1:B:519:MET:CE	2.49	0.42
1:A:260:LEU:HD13	1:A:506:PHE:CG	2.54	0.42
1:A:275:HIS:HA	1:A:279:VAL:CG2	2.50	0.42
1:B:297:GLN:OE1	1:B:328:VAL:HG22	2.19	0.42
1:A:532:ARG:HH22	1:B:530:VAL:HG12	1.85	0.42
1:B:513:ILE:HB	1:B:514:PRO:HD3	2.01	0.42
1:B:275:HIS:HA	1:B:279:VAL:HG23	2.02	0.41
1:A:233:MET:HE3	1:A:505:GLU:HB3	2.03	0.41
1:A:272:ILE:O	1:A:276:ILE:HG13	2.20	0.41
1:B:209:THR:HG21	1:B:519:MET:HE2	2.02	0.41
1:A:166:LEU:HD12	1:B:170:ARG:NH2	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	499/543 (92%)	479 (96%)	17 (3%)	3 (1%)	25	47
1	B	496/543 (91%)	474 (96%)	19 (4%)	3 (1%)	25	47
All	All	995/1086 (92%)	953 (96%)	36 (4%)	6 (1%)	29	47

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	118[A]	GLN
1	B	118[B]	GLN
1	A	31	ARG
1	A	80	GLU
1	B	80	GLU
1	A	453	ARG

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	421/449 (94%)	411 (98%)	10 (2%)	49	74
1	B	418/449 (93%)	410 (98%)	8 (2%)	57	79
All	All	839/898 (93%)	821 (98%)	18 (2%)	52	77

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

Mol	Chain	Res	Type
1	A	50	LEU
1	A	70	ARG
1	A	100	ASP
1	A	108	GLN
1	A	116	GLU
1	A	206	MET
1	A	337	VAL
1	A	420	SER
1	A	489	THR
1	A	530	VAL
1	B	99	ASP
1	B	111	ARG
1	B	135	ARG
1	B	206	MET
1	B	241	LYS
1	B	281	GLU
1	B	282	ASP
1	B	440	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	GLN
1	A	504	GLN
1	B	74	GLN
1	B	108	GLN
1	B	180	GLN
1	B	309	ASN

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 15 ligands modelled in this entry, 12 are monoatomic - leaving 3 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	$\# Z > 2$
5	MES	A	570	-	12,12,12	1.86	1 (8%)	14,16,16	1.99	4 (28%)
4	ADP	B	562	2	24,29,29	0.91	1 (4%)	29,45,45	1.23	3 (10%)
4	ADP	A	562	2	24,29,29	0.87	0	29,45,45	1.35	2 (6%)

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
5	MES	A	570	-	-	4/6/14/14	0/1/1/1
4	ADP	B	562	2	-	0/12/32/32	0/3/3/3
4	ADP	A	562	2	-	0/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	570	MES	C8-S	-6.04	1.68	1.77
4	B	562	ADP	C5-C4	2.25	1.46	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	562	ADP	N3-C2-N1	-4.47	121.69	128.68
5	A	570	MES	O1S-S-C8	3.73	111.41	106.92
5	A	570	MES	C5-N4-C3	3.67	117.08	108.83
4	B	562	ADP	N3-C2-N1	-3.25	123.59	128.68
5	A	570	MES	O2S-S-C8	3.12	110.68	106.92
4	B	562	ADP	PA-O3A-PB	-2.78	123.29	132.83
4	B	562	ADP	N6-C6-N1	2.33	123.42	118.57
4	A	562	ADP	C3'-C2'-C1'	2.13	104.19	100.98
5	A	570	MES	O2S-S-O1S	-2.10	106.67	113.95

There are no chirality outliers.

All (4) torsion outliers are listed below:

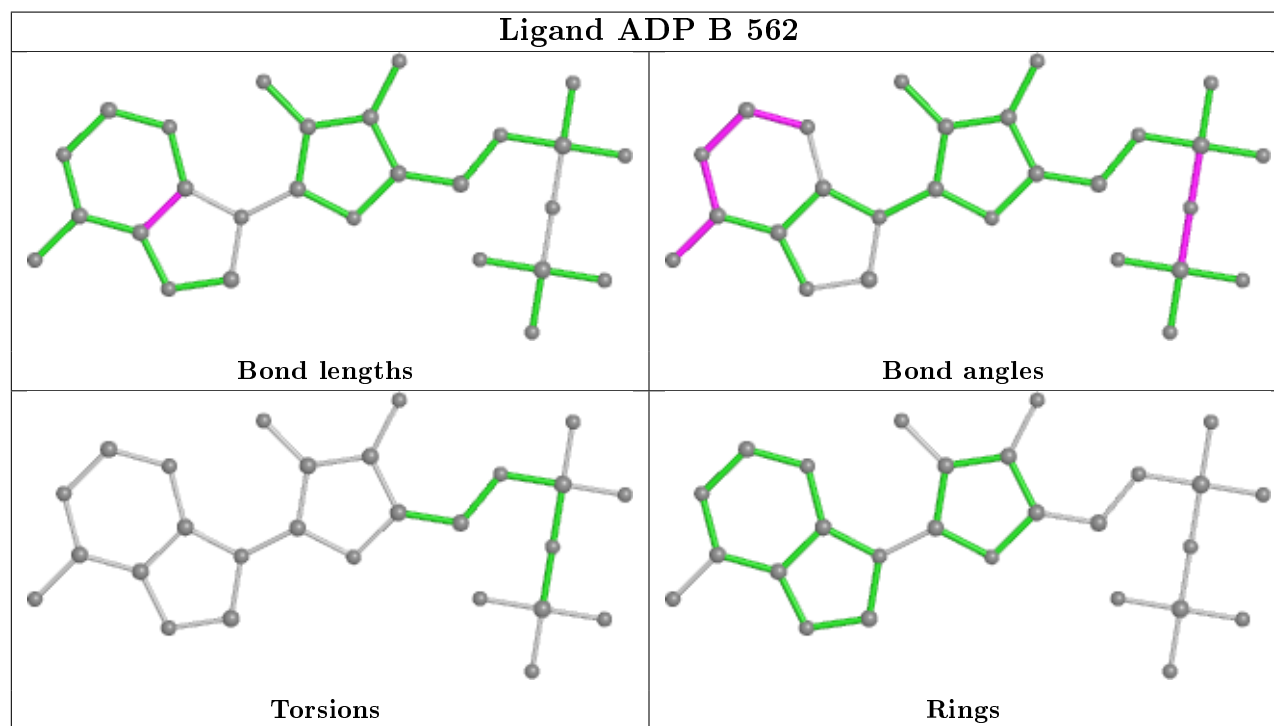
Mol	Chain	Res	Type	Atoms
5	A	570	MES	C7-C8-S-O1S
5	A	570	MES	C7-C8-S-O3S
5	A	570	MES	C8-C7-N4-C3
5	A	570	MES	C7-C8-S-O2S

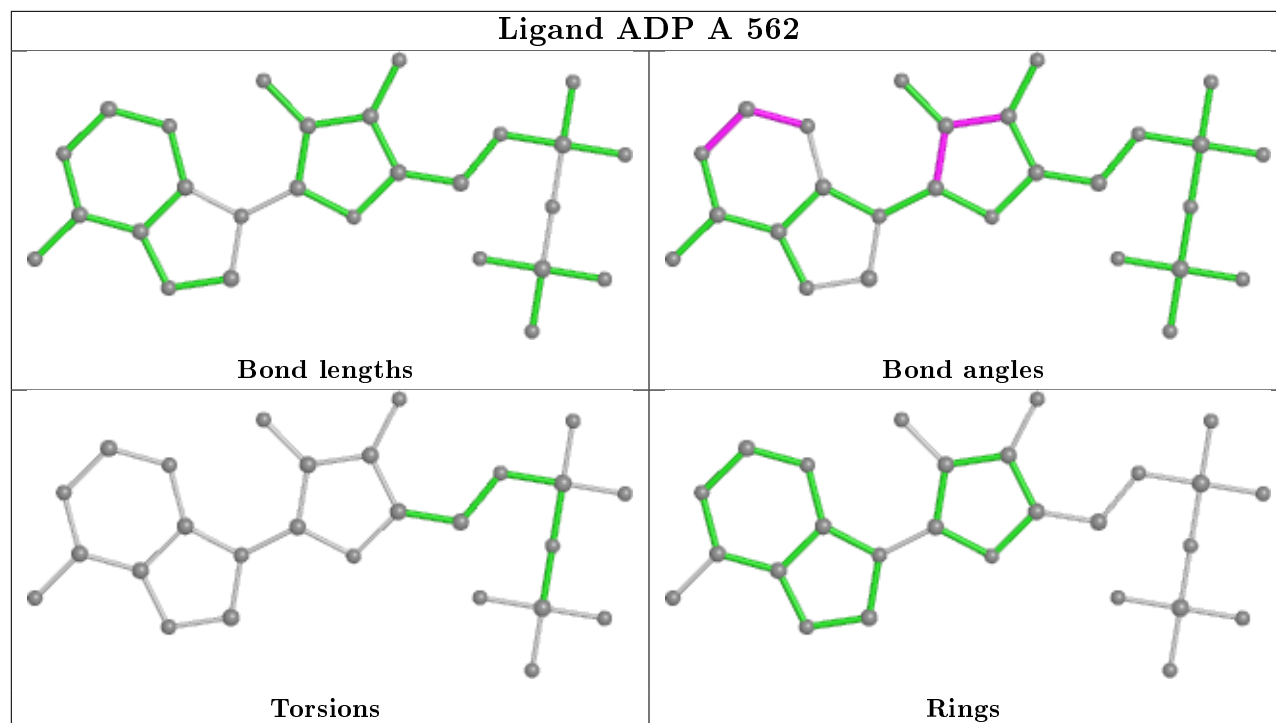
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	562	ADP	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	499/543 (91%)	-0.03	19 (3%)	40 33	28, 39, 56, 84	0
1	B	496/543 (91%)	0.04	34 (6%)	16 12	28, 39, 54, 72	0
All	All	995/1086 (91%)	0.01	53 (5%)	26 20	28, 39, 55, 84	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	474	ARG	6.9
1	B	141	GLY	5.8
1	B	140	ASP	5.5
1	A	483	ASP	5.2
1	B	30	SER	4.5
1	B	282	ASP	4.3
1	B	33	ARG	4.2
1	A	489	THR	4.2
1	B	489	THR	4.1
1	A	482	GLN	4.0
1	B	139	GLY	4.0
1	B	414	ASP	4.0
1	B	341	ALA	4.0
1	A	481	ILE	4.0
1	A	30	SER	3.9
1	B	532	ARG	3.4
1	A	33	ARG	3.4
1	B	342	GLY	3.4
1	B	487	PHE	3.2
1	A	479	LYS	3.2
1	A	474	ARG	3.1
1	A	491	LYS	3.1
1	B	440	ASP	3.1
1	A	533	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	473	SER	2.8
1	B	497	LYS	2.8
1	B	476	VAL	2.7
1	A	480	ASN	2.7
1	A	490	VAL	2.7
1	B	283	ASN	2.7
1	B	280	ASP	2.7
1	B	472	ASP	2.6
1	A	56	LEU	2.6
1	B	488	SER	2.6
1	B	118[A]	GLN	2.5
1	B	533	PRO	2.5
1	A	283	ASN	2.5
1	A	140	ASP	2.3
1	A	282	ASP	2.3
1	B	120	GLN	2.3
1	B	475	THR	2.2
1	B	52	GLU	2.2
1	B	281	GLU	2.2
1	B	31	ARG	2.2
1	B	453	ARG	2.2
1	B	433	GLU	2.1
1	A	31	ARG	2.1
1	A	101	ALA	2.1
1	B	127	ASP	2.1
1	B	80	GLU	2.0
1	B	343	GLN	2.0
1	A	72	PHE	2.0
1	B	279	VAL	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 ⓘ

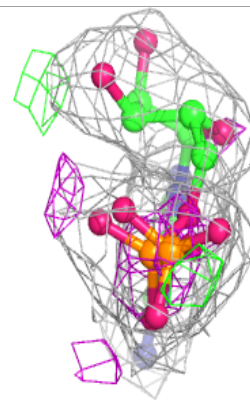
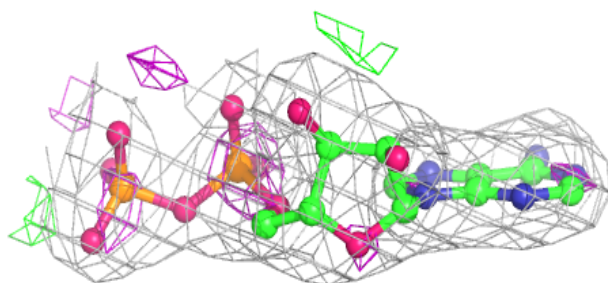
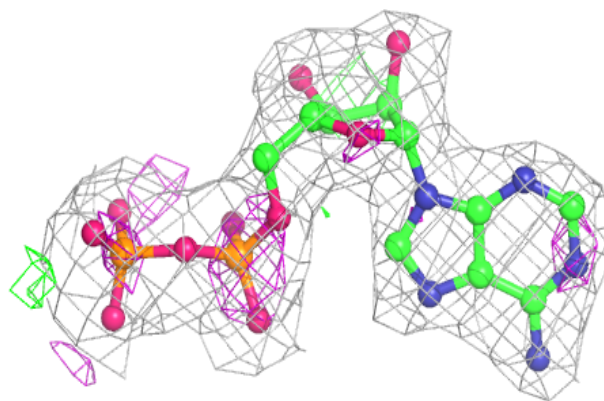
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MES	A	570	12/12	0.84	0.26	69,70,72,72	0
2	MG	B	563	1/1	0.94	0.13	53,53,53,53	0
2	MG	A	563	1/1	0.96	0.10	43,43,43,43	0
3	CL	A	567	1/1	0.96	0.17	38,38,38,38	0
3	CL	A	569	1/1	0.97	0.37	41,41,41,41	0
3	CL	B	567	1/1	0.97	0.21	33,33,33,33	0
3	CL	B	566	1/1	0.97	0.05	46,46,46,46	0
3	CL	B	568	1/1	0.97	0.22	52,52,52,52	0
3	CL	B	569	1/1	0.98	0.17	42,42,42,42	0
4	ADP	A	562	27/27	0.98	0.08	32,34,36,36	0
3	CL	B	565	1/1	0.98	0.10	41,41,41,41	0
4	ADP	B	562	27/27	0.98	0.08	28,34,36,38	0
2	MG	A	564	1/1	0.98	0.04	32,32,32,32	0
2	MG	B	564	1/1	0.99	0.02	32,32,32,32	0
3	CL	A	566	1/1	0.99	0.12	41,41,41,41	0

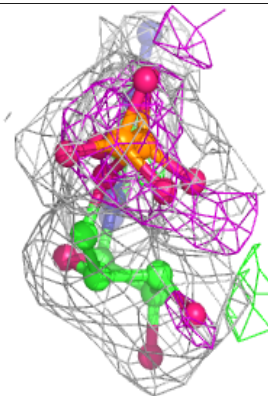
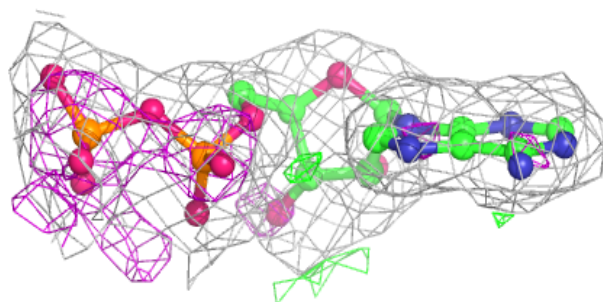
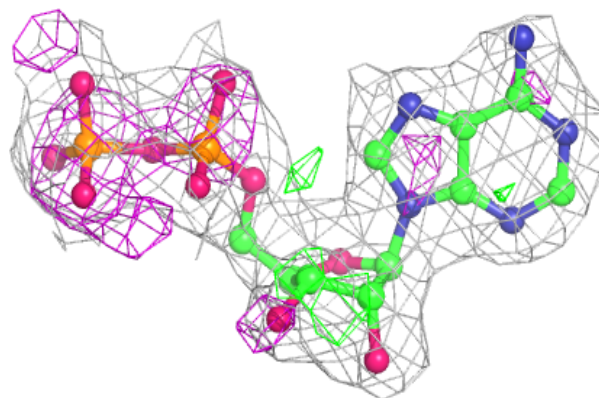
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP A 562:

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

**Electron density around ADP B 562:**

$2mF_o-DF_c$ (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.